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FIGURE 438

MWLPLGLLSLCLSPILSSPSLKSQACQQLLWTLPSPLVAFRANRTTYVMDVSTNQSGMEH
RNHLCFCDLYDRATSPPLKCSLL

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FIGURE 439

GTTTCTCATAGTTGGCGTCTTCTAAAGGAAAAACACTAAAATGAGGAACTCAGCGGACCGGGAGCGACGCAGCTT
GAGGGAAGCATCCCTAGCTGTTGGCGCAGAGGGGCGAGGCTGAAGCCGAGTGGCCCGAGGTGTCTGAGGGGCTGG
GGCAAAGGTGAAAGAGTTTCAGAACAAAGCTTCCTGGAACCCATGACCCATGAAGTCTTGTGACATTTATACCGT
CTGAGGGTAGCAGCTCGAAACTAGAAGAAGTGGAGTGTGCCAGGGACGGCAGTATCTCTTTGTGTGACCCCTGGC
GGCCTATGGGACGTTGGCTTCAGACCTTTGTGATACACCATGCTGCGTGGGACGATGACGGCGTGGAGAGGAATG
AGGCCTGAGGTCACACTGGCTTGCTCCTCCTAGCCACAGCAGGCTGCTTTGCTGACTTGAACGAGGTCCCTCAG
GTCACCGTCCAGCCTGCGTCCACCGTCCAGAAGCCCGGAGGCACTGTGATCTTGGGCTGCGTGGTGGAACTCCA
AGGATGAATGTAACCTGGCGCTGAATGGAAAGGAGCTGAATGGCTCGGATGATGCTCTGGGTGTCCTCATCACC
CACGGGACCCCTCGTCATCACTGCCCTTAACAACCACTGTGGGACGGTACCAGTGTGTGGCCCGGATGCCTGCG
GGGCTGTGGCCAGCGTGCCAGCCACTGTGACACTAGCCAATCTCCAGGACTTCAAGTTAGATGTGCAGCACGTG
ATTGAAGTGGATGAGGGAAACACAGCAGTCAATTGCTGCCACCTGCCTGAGAGCCACCCCAAAGCCAGGTCCGG
TACAGCGTCAAACAAGAGTGGCTGGAGGCCTCCAGAGGTAACCTGATCATGCCCTCAGGGAACTCCAGATT
GTGAATGCCAGCCAGGAGGACGAGGGCATGTACAAGTGTGCAGCCTACAACCCAGTGACCCAGGAAGTGAAACC
TCCGGCTCCAGCGACAGGCTACGTGTGCGCCGCTCCACCGCTGAGGCTGCCCGCATCATCTACCCCCCAGAGGCC
CAAACCATCATCGTCACCAAAGGCCAGAGTCTCATTCTGGAGTGTGTGGCCAGTGGAAATCCACCCCCACGGGTC
ACCTGGGCCAAGGATGGGTCCAGTGTACCGGCTACAACAAGACGCGCTTCTGCTGAGCAACCTCCTCATCGAC
ACCACGAGGAGGAGTCAAGCAGCTACCGCTGACCTGAGGCTGACCAATGGGCTTGGGCGAGCCCGGCGAGCGGTC
ATCCTCTACAATGTCCAGGTGTTTGAACCCCTGAGGTACCATGGAGCTATCCAGCTGGTTCATCCCTGGGGC
CAGAGTGCCAAAGCTTACCTGTGAGGTGCGTGGGAACCCCCGCCCTCCGTGCTGTGGCTGAGGAATGCTGTGCC
CTCATCTCCAGCCAGCGCCTCCGGCTCTCCCGCAGGGCCCTGCGCGTGTCTCAGCATGGGGCCTGAGGACGAAGGC
GTCTACCAGTGCATGGCCGAGAACGAGGTTGGGAGCGCCCATGCCGTAGTCCAGCTGCGGACCTCCAGGCCAAGC
ATAACCCCAAGGCTATGGCAGGATGCTGAGCTGGCTACTGGCACACCTCCTGTATCACCTCCAACTCGGCAAC
CCTGAGCAGATGCTGAGGGGGCAACCGGCGCTCCCCAGACCCCAACGTCAAGTGGGGCCTGCTTCCCCGAAGTGT
CCAGGAGAGAAGGGGAGGGGGCTCCCGCCGAGGCTCCCATCATCCTCAGCTCGCCCCGCACCTCCAAGACAGAC
TCATATGAACTGGTGTGGCGGCTCGGCATGAGGGCAGTGGCCGGGCGCCAATCCTCTACTATGTGGTGAAACAC
CGCAAGCAGGTACAAATTCCTCTGACGATTGGACCATCTCTGGCATTCCAGCCAACAGCACCAGCTGACCTC
ACCAGACTTGACCCCGGAGCTTGTATGAAGTGGAGATGGCAGCTTACAAGTGTGCGGGAGAGGGCCAGACAGCC
ATGGTCACCTTCCGAAGTGGACGGCGGCCAAACCCGAGATCATGGCCAGCAAAGAGCAGCAGATCCAGAGAGAC
GACCCTGGAGCCAGTCCCCAGAGCAGCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCCAGCC
CCCACCATCTCCACGGCCTCCGAGACCTCAGTGTACGTGACCTGGATTCCCCGTGGGAATGGTGGGTTCCTAATC
CAGTCTTCCGTGTGGAGTACAAGAAGCTAAAGAAAGTGGGAGACTGGATTCTGGCCACCAGCGCCATCCCCCA
TCGCGGCTGTCCGTGGAGATCACGGGCTAGAGAAAGGCACCTCCTACAAGTTTCGAGTCCGGGCTCTGAACATG
CTGGGGGAGAGCGAGCCAGCGCCCCCTCTCGGCCCTACGTGGTGTGGGGCTACAGCGGTGCGGTGTACGAGAGG
CCCCTGGCAGGTCTTTATATCACCTTCACGGATGCGGTCAATGAGACCACCATCATGCTCAAGTGGATGTACATC
CCAGCAAGTAACAACAACACCCCAATCCATGGCTTTTATATCTATTATCGACCCACAGACAGTGAATGATAGT
GACTACAAGAAGGATATGGTGGAAAGGGGACAAGTACTGGCACTCCATCAGCCACCTGCAGCCAGAGACCTCCTAC
GACATTAAGATGCAGTGTCTCAATGAAGGAGGGGAGAGCGAGTTCAGCAACGTGATGATCTGTGAGACCAAAGCT
CGGAAGTCTTCTGGCCAGCCTGGTGCAGTGGCACCCTCACTCTGGCCCCACACAGCCGCCCCCTTCTGAAACC
ATAGAGCGGCGGTGGGCAGTGGGGCCATGGTGGCTCGCTCCAGCGACCTGCCCTATCTGATTGTGGGGTCTGTC
CTGGGCTCCATCGTTCTCATCATCGTCACCTTCATCCCTTCTGCTTGTGGAGGGCCTGGTCTAAGCAAAAACAT
ACAACAGACCTGGGTTTTCTCGAAGTGCCCTTCACCCCTCCTGCCCCGATATACTATGGTGCCATTGGGAGGACTC
CCAGGCCACCAGGCCAGTGGACAGCCCTACCTCAGTGGCATCAGTGGACGGGCTGTGCTAATGGGATCCACATG
AATAGGGGCTGCCCCCTCGGCTGCAGTGGGCTACCCGGGCATGAAGCCCCAGCAGCACTGCCAGGCGAGCTTCAG
CAGCAGAGTGACACCAGCAGCCTGCTGAGGCAGACCCATCTTGGCAATGGATATGACCCCAAGTCAACAGATC
ACGAGGGGTCCCAAGTCTAGCCCGGACGAGGGCTCTTTCTTATACACACTGCCCCGACGACTCCACTCACCAGCTG
CTGCAGCCCCATCAGCACTGCTGCCAACGCCAGGAGCAGCCTGCTGCTGTGGGCCAGTCAGGGGTGAGGAGAGCC
CCCGACAGTCTGTCTTGAAGCAGTGTGGGACCCTCCATTTCACTCAGGGGCCCCCATGCTGCTTGGGCTTGTG
CCAGTTGAAGAGGTGGACAGTCTGACTCCTGCCAAGTGAGTGGAGGAGACTGGTGTCCCCAGCACCCCGTAGGG
GCCTACGTAGGACAGGAACCTGGAATGCAGCTCTCCCCGGGGCCACTGGTGGCTGTGTCTTTTGAAACACCACCT
CTCACAATTTAGGCAGAAAGCTGATATCCAGAAAGACTATATATTGTTTTTTTTTAAAAAAGAGAAAAA
AGAGACAGAGAAAATTGGTATTTATTTTCTATTATAGCCATATTTATATATTATGCACTTGTAATAAATGTA
TATGTTTTATAATTCTGGAGAGACATAAGGAGTCTACCCGTTGAGGTTGGAGAGGGGAAATAAAGAGCTGCCA
CCTAACAGGAGTCAACCAGGAAAGCACCGCACAGGCTGGCGCGGGACAGACTCCTAACCTGGGGCTCTGCAGTG
GCAGGCGAGGCTGCAGGAGGCCACAGATAAGCTGGCAAGAGGAAGGATCCAGGCACATGGTTTCATCAGAGCA
TGAGGGAACAGCAAGGGGACGGTATCACAGCCTGGAGACACCCACACAGATGGCTGGATCCGGTGTACGGGAA
ACATTTTCTAAGATGCCCATGAGAACAGACCAAGATGTGTACAGCACTATGAGCATTAATAAACCTTCAGAAAT
CAATAATCCGTGGCAACATATCTCTGTAAAAACAAACACTGTAACCTCTAAATAAATGTTTAGTCTTCCCTGTAAAA

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FIGURE 440

MLRGTMTAWRGMRPEVTLACLLLATAGCFADLNEVPQVTVQPASTVQKPGGTVILGCVVEPPR
MNVTWRLNGKELNGSDDALGVLITHGTLVITALNNHTVGRYQCVARMPAGAVASVPATVTLAN
LQDFKLDVQHVIEVDEGNTAVIACHLPESHKPAQVRYSVKQEWLEASRGNYLIMPSGNLQIVN
ASQEDEGMYKCAAYNPVTQEVKTSGSSDRLRVRRSTAEAAARI IYPPEAQTIIVTKGQSLILEC
VASGIPPPRVTWAKDGSSVTGYNKTRFLLSNLLIDTTSEEDSGTYRCMADNGVGQPGA AVILY
NVQVFEPPEVTMELS QLVI PWGQSAKLTCEVRGNPPPSVLWLRNAVPLISSQRLRLSRRALRV
LSMGPEDEGVYQCMAENEVGSAHAVVQLRTSRPSITPRLWQDAELATGTPPVSPSKLGNPEQM
LRGQPALPRPPTSVGPASPKCPGKQGA PAEAPIILSSPRTSKTDSYELVWRPRHEGSGRAP
ILYVVKHRKQVTNSSDDWTISGIPANQHRLTLTRLDPGSLYEVEMAAYNCAGEGQTAMVTFR
TGRRPKPEIMASKEQQIQRDDPGAS PQSSSQPDHGRLSPPEAPDRPTISTASETSVYVTWIPR
GNGGFPIQSFRVEYKKLKKVGDWILATSAIPPSRLSVEITGLEKGT SYKFRVRALNMLGESEP
SAPSRPYVVGYSGRVYERP VAGPYITFTDAVNETTIMLKWMI PASNNNTPIHGFYIYYRPT
DSDNDSYKKDMVEGD KYWHSISHLQPETSYDIKMQCFNEGGESEFSNVMICETKARKSSGQP
GRLPPPTLAPPQPPLPETIERPVGTGAMVARSSDLPYLIVGVVLGSI VLIIVTFIPFCLWRAW
SKQKHTTDLGFPRSALPPSCPYTMVPLGGLPGHQASGQPYLSGISGRACANGIHMNRGCPSAA
VGYPGMKPQQHCPGELQQQSDTSSLLRQTHLGNGYDPQSHQITRGPKSSPDEGSFLYTL PDDS
THQLLQPHHDCCQRQEQPAAVGQSGVRRAPDSPVLEAVWDP PFHSGPPCCLGLVPVEEVDS PD
SCQVSGGDWCPQHVPVGAYVGQEPGMQLSPGPLVRVSFETPPLTI

Signal peptide:
amino acids 1-30

Transmembrane domain:
amino acids 16-30 (type II), 854-879

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FIGURE 441

GAGAGAATAGCTACAGATTCTCCATCCTCAGTCTTTGCAAGGCGACAGCTGTGCCAGCCGGGC
TCTGGCAGGCTCCTGGCAGCATGGCAGTGAAGCTTGGGACCCTCCTGCTGGCCCTTGCCCTGG
GCCTGGCCCAGCCAGCCTCTGCCCCGCCGAAGCTGCTGGTGTTTCTGCTGGATGGTTTTCTGCT
CAGACTACATCAGTGATGAGGCGCTGGAGTCATTGCCTGGTTTCAAAGAGATTGTGAGCAGGG
GAGTAAAAGTGGATTACTTGACTCCAGACTTCCCTAGTCTCTCGTATCCCAATTATTATACCC
TAATGACTGGCCGCCATTGTGAAGTCCATCAGATGATCGGGAACTACATGTGGGACCCACCA
CCAACAAGTCCTTTGACATTGGCGTCAACAAAGACAGCCTAATGCCTCTCTGGTGGAATGGAT
CAGAACCTCTGTGGGTCACTCTGACCAAGGCCAAAAGGAAGGTCTACATGTACTACTGGCCAG
GCTGTGAGGTTGAGATTCTGGGTGTCAGACCCACCTACTGCCTAGAATATAAAAATGTCCCAA
CGGATATCAATTTTGCCAATGCAGTCAGCGATGCTCTTGACTCCTTCAAGAGTGGCCGGGCCG
ACCTGGCAGCCATATACCATGAGCGCATTGACGTGGAAGGCCACCACTACGGGCCTGCATCTC
CGCAGAGGAAAGATGCCCTCAAGGCTGTAGACACTGTCCTGAAGTACATGACCAAGTGGATCC
AGGAGCGGGGCCTGCAGGACCGCCTGAACGTCATTATTTTCTCGGATCACGGAATGACCGACA
TTTTCTGGATGGACAAAGTGATTGAGCTGAATAAGTACATCAGCCTGAATGACCTGCAGCAAG
TGAAGGACCGCGGGCCTGTTGTGAGCCTTTGGCCGGCCCTGGGAAACACTCTGAGATATATA
ACAAACTGAGCACAGTGGAACACATGACTGTCTACGAGAAAGAAGCCATCCCAAGCAGGTTCT
ATTACAAGAAAGGAAAGTTTGTCTCTCCTTTGACTTTAGTGGCTGATGAAGGCTGGTTCATAA
CTGAGAATCGAGAGATGCTTCCGTTTTGGATGAACAGCACCGGCAGGCGGGAAGGTTGGCAGC
GTGGATGGCACGGCTACGACAACGAGCTCATGGACATGCGGGGCATCTTCCTGGCCTTCGGAC
CTGATTTCAAATCCAACCTTCAGAGCTGCTCCTATCAGGTGGTGGACGTCTACAATGTCATGT
GCAATGTGGTGGGCATCACCCCGCTGCCCAACAACGGATCCTGGTCCAGGGTGATGTGCATGC
TGAAGGGCCGCGCCGGCACTGCCCCGCCTGTCTGGCCCAGCCACTGTGCCCTGGCACTGATTC
TTCTCTTCCTGCTTGCATAACTGATCATATTGCTTGTCTCAGAAAAAACACCATCAGCAAAG
TGGGCCTCCAAAGCCAGATGATTTTCATTTTATGTGTGAATAATAGCTTCATTAACACAATCA
AGACCATGCACATTGTAAATACATTATTCTTGGATAATTCTATACATAAAAGTTCCTACTTGT
TAAA

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FIGURE 442

MAVKLGTTTTLLALALGLAQPASARRKLLVFLLDGFRSDYISDEALESPLPGFKEIVSRGVKVDYL
TPDFPSLSYPNYYTLMTGRHCEVHQMIGNYMWDPTTNKSFDIGVNKDSLMLPLWWNGSEPLWVT
LTKAKRKVYMYWPGCEVEILGVRPTYCLEYKNVPTDINFANAVSDALDSFKSGRADLAAIYH
ERIDVEGHHYGPASPQRKDALKAVDTVLKYMTKWIQERGLQDRNLNVIIFSDHGMTDIFWMDKV
IELNKYISLNDLQQVKDRGPVVSLLWPAPGKHSEIYNKLSTVEHMTVYEKEAIPSRFYKKGKF
VSPLTLVADEGWFITENREMLPFWMNSTGRREGWQRGWHGYDNELMDMRGIFLAFGPDFKSNF
RAAPIRSVDVYNVMCNVVGITPLPNNGSWSRVMCMLKGRAGTAPPVWPSHCALALILLFLLA

Important features of the protein:**Signal peptide:**

amino acids 1-22

N-glycosylation sites.

amino acids 100-104, 118-122, 341-345, 404-408

N-myristoylation sites.

amino acids 148-154, 365-371

Amidation site.

amino acids 343-347

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FIGURE 443

AGTGACTGCAGCCTTCCTAGATCCCCTCCACTCGGTTTCTCTCTTTGCAGGAGCACCGGCAGC
ACCAGTGTGTGAGGGGAGCAGGCAGCGGTCCTAGCCAGTTCCTTGATCCTGCCAGACCACCCA
GCCCCCGGCACAGAGCTGCTCCACAGGCACCA**ATG**AGGATCATGCTGCTATTCACAGCCATCCT
GGCCTTCAGCCTAGCTCAGAGCTTTGGGGCTGTCTGTAAGGAGCCACAGGAGGAGGTGGTTCC
TGGCGGGGGCCGCAGCAAGAGGGATCCAGATCTCTACCAGCTGCTCCAGAGACTCTTCAAAG
CCACTCATCTCTGGAGGGATTGCTCAAAGCCCTGAGCCAGGCTAGCACAGATCCTAAGGAATC
AACATCTCCCGAGAAACGTGACATGCATGACTTCTTTGTGGGACTTATGGGCAAGAGGAGCGT
CCAGCCAGAGGGAAAGACAGGACCTTTCTTACCTTCAGTGAGGGTTCTCTCGGCCCTTCATCC
CAATCAGCTTGGATCCACAGGAAAGTCTTCCCTGGGAACAGAGGAGCAGAGACCTTTA**TAA**GA
CTCTCCTACGGATGTGAATCAAGAGAACGTCCCCAGCTTTGGCATCCTCAAGTATCCCCCGAG
AGCAGAATAGGTACTCCACTTCCGGACTCCTGGACTGCATTAGGAAGACCTCTTTCCCTGTCC
CAATCCCCAGGTGCGCACGCTCCTGTTACCCTTTCTCTTCCCTGTTCTTGTAACATTCTTGTC
CTTTGACTCCTTCTCCATCTTTTCTACCTGACCCTGGTGTGGAACTGCATAGTGAATATCCC
CAACCCCAATGGGCATTGACTGTAGAATACCCTAGAGTTCCTGTAGTGTCTTACATTAAAAAT
ATAATGTCTCTCTCTATTCTCAACAATAAAGGATTTTGCATATGAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 444

MRIMLLFTAILAFSLAQSFQAVCKEPQEEVVPGGGRSKRDPDLYQLLQRLFKSHSSLEGLLKA
LSQASTDPKESTSPEKRDMHDFVGLMGKRSVQPEGKTGPFLPSVRVPRPLHPNQLGSTGKSS
LGTEEQRPL

Important features:**Signal peptide:**

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 36-45

N-myristoylation site.

amino acids 33-39, 59-65

Amidation site.

amino acids 90-94

Leucine zipper pattern.

amino acids 43-65

Tachykinin family signature.

amino acids 86-92

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FIGURE 445

TGGACTTCTCTGGACCACAGTCCTCTGCCAGACCCCTGCCAGACCCCAGTCCACCATGATCCATCTGGGTCACAT
CCTCTTCCTGCTTTTGCTCCCAGTGGCTGCAGCTCAGACGACTCCAGGAGAGAGATCATCACTCCCTGCCTTTTA
CCCTGGCACTTCAGGCTCTTGTTCCGGATGTGGGTCCCTCTCTCTGCCGCTCCTGGCAGGCCTCGTGGCTGCTGA
TGCGGTGGCATCGCTGCTCATCGTGGGGGCGGTGTTCTGTGCGCACGCCCAGCCGCAGCCCCGCCCAAGATGG
CAAAGTCTACATCAACATGCCAGGCAGGGGCTGACCCCTCCTGCAGCTTGGACCTTTGACTTCTGACCCTCTCATC
CTGGATGGTGTGTGGTGGCACAGGAACCCCGCCCCAACTTTTGGATTGTAATAAAACAATTGAAACACCA

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FIGURE 446

MIHLGHILFLLLLPVAAAQTTPGERSSLPAFYPGTSGSCSGCSLSLPLLAGLVAADAVASLLIVGAVFLCARPR
RSPAQDGKVYINMPGRG

Signal peptide:	Amino acids 1-18
transmembrane domain:	Amino acids 51-70
Glycosaminoglycan attachment site:	Amino acids 40-44
N-myristoylation sites:	Amino acids 34-40;37-43;52-58
Prokaryotic membrane lipoprotein lipid attachment site:	Amino acids 29-40

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FIGURE 447

GCCAGGTGTGCAGGCCGCTCCAAGCCCAGCCTGCCCCGCTGCCGCCACCATGACGCTCCTCCC
CGGCCTCCTGTTTCTGACCTGGCTGCACACATGCCTGGCCCACCATGACCCCTCCCTCAGGGG
GCACCCCCACAGTCACGGTACCCACACTGCTACTCGGCTGAGGAACTGCCCTCGGCCAGGC
CCCCCACACCTGCTGGCTCGAGGTGCCAAGTGGGGGCAGGCTTTGCCTGTAGCCCTGGTGTC
CAGCCTGGAGGCAGCAAGCCACAGGGGGAGGCACGAGAGGCCCTCAGCTACGACCCAGTGCCC
GGTGCTGCGGCCGGAGGAGGTGTTGGAGGCAGACACCCACCAGCGCTCCATCTCACCCCTGGAG
ATACCGTGTGGACACGGATGAGGACCGCTATCCACAGAAGCTGGCCTTCGCCGAGTGCCCTGTG
CAGAGGCTGTATCGATGCACGGACGGGCCGCGAGACAGCTGCGCTCAACTCCGTGCGGCTGCT
CCAGAGCCTGCTGGTGCTGCGCCGCCGGCCCTGCTCCCGCGACGGCTCGGGGCTCCCCACACC
TGGGGCCTTTGCCTTCCACACCGAGTTCATCCACGTCCCCGTCGGCTGCACCTGCGTGCTGCC
CCGTTCAGTGTGACCGCCGAGGCCGTGGGGCCCCCTAGACTGGACACGTGTGCTCCCCAGAGGG
CACCCCTATTTATGTGTATTTATTGTTATTTATATGCCTCCCCAACACTACCCTTGGGGTC
TGGGCATTCCCCGTGTCTGGAGGACAGCCCCCACTGTTCTCCTCATCTCCAGCCTCAGTAGT
TGGGGGTAGAAGGAGCTCAGCACCTCTTCCAGCCCTTAAAGCTGCAGAAAAGGTGTCACACGG
CTGCCTGTACCTTGGCTCCCTGTCCTGCTCCCGGCTTCCCTTACCCTATCACTGGCCTCAGGC
CCCGCAGGCTGCCTCTTCCCAACCTCCTTGGAAGTACCCCTGTTTCTTAAACAATTATTAAAG
TGTACGTGTATTATTAAACTGATGAACACATCCCCAAA

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FIGURE 448

MTLLPGLLFLTWLHTCLAHHDPSLRGHPHSHGTPHCYSAEELPLGQAPPHELLARGAKWGQALP
VALVSSLEAASHRGRHERPSATTQCPVLRPEEVLEADTHQRSISPWRVYRVDTDEDYPQKLAF
AECLCRGCIDARTGRETAALNSVRLQLSLLVLRRRPCSRDGSGLPTPGAFAFHTEFIHVPVGC
TCVLPRSV

Important features:

Signal peptide:

amino acids 1-18

Tyrosine kinase phosphorylation site.

amino acids 112-121

N-myristoylation sites.

amino acids 32-38, 55-61, 133-139

Leucine zipper pattern.

amino acids 3-25

Homologous region to IL-17.

amino acids 99-195

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FIGURE 449

TGCAGAGCTTGTGGAGGCCATGGGGCGCGTCGTCGCGGAGCTCGTCTCCTCGCTGCTGGGGTT
GTGGCTGTTGCTGTGCAGCTGCGGATGCCCCGAGGGCGCCGAGCTGCGTGCTCCGCCAGATAA
AATCGCGATTATTGGAGCCGGAATTGGTGGCACTTCAGCAGCCTATTACCTGCGGCAGAAATT
TGGGAAAGATGTGAAGATAGACCTGTTTGAAAGAGAAGAGGTCGGGGGCGCCCTGGCTACCAT
GATGGTGCAGGGGCAAGAATACGAGGCAGGAGGTTCTGTCATCCATCCTTTAAATCTGCACAT
GAAACGTTTTGTCAAAGACCTGGGTCTCTCTGCTGTTTCAGGCCTCTGGTGGCCTACTGGGGAT
ATATAATGGAGAGACTCTGGTATTTGAGGAGAGCAACTGGTTCATAATTAACGTGATTAAATT
AGTTTGGCGCTATGGATTTCAATCCCTCCGTATGCACATGTGGGTAGAGGACGTGTTAGACAA
GTTTCATGAGGATCTACCGCTACCAGTCTCATGACTATGCCTTCAGTAGTGTCGAAAAATTACT
TCATGCTCTAGGAGGAGATGACTTCCTTGGAATGCTTAATCGAACACTTCTTGAAACCTTGCA
AAAGGCCGGCTTTTCTGAGAAGTTCCTCAATGAAATGATTGCTCCTGTTATGAGGGTCAATTA
TGGCCAAAGCACGGACATCAATGCCTTTGTGGGGGCGGTGTCACCTGTCCTGTTCTGATTCTGG
CCTTTGGGCAGTAGAAGGTGGCAATAAACTTGTTTGCTCAGGGCTTCTGCAGGCATCCAAAAG
CAATCTTATATCTGGCTCAGTAATGTACATCGAGGAGAAAACAAAGACCAAGTACACAGGAAA
TCCAACAAAGATGTATGAAGTGGTCTACCAAATTGGAAGTGAAGTCTGTTTCAGACTTCTATGA
CATCGTCTTGGTGGCCACTCCGTTGAATCGAAAAATGTCGAATATTACTTTTCTCAACTTTGA
TCCTCCAATTGAGGAATTCCATCAATATTATCAACATATAGTGACAACTTTAGTTAAGGGGGA
ATTGAATACATCTATCTTTAGCTCTAGACCCATAGATAAATTTGGCCTTAATACAGTTTTAAC
CACTGATAATTCAGATTTGTTTCATTAACAGTATTGGGATTGTGCCCTCTGTGAGAGAAAAGGA
AGATCCTGAGCCATCAACAGATGGAACATATGTTTGGAAGATCTTTTCCCAAGAACTCTTAC
TAAAGCACAAATTTTAAAGCTCTTTCTGTCTCTATGATTATGCTGTGAAGAAGCCATGGCTTGC
ATATCCTCACTATAAGCCCCCGAGAAATGCCCTCTATCATTCTCCATGATCGACTTTATTA
CCTCAATGGCATAGAGTGTGCAGCAAGTGCCATGGAGATGAGTGCCATTGCAGCCCACAACGC
TGCACTCCTTGCCATACACCGCTGGAACGGGCACACAGACATGATTGATCAGGATGGCTTATA
TGAGAACTTAAACTGAAGTATGAAGTGAACACTCCTTTTTCCCTCCTAGTTCCAAATGA
CTATCAGTGGCAAAAAAGAACAAAATCTGAGCAGAGATGATTTTGAACCAGATATTTTGCCAT
TATCATTGTTTAATAAAAGTAATCCCTGCTGGTCATAGGAAAAAAAAAAAAA

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FIGURE 450

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA62880
<subunit 1 of 1, 505 aa, 1 stop
<MW: 56640, pI: 6.10, NX(S/T): 4
MGRVVAELVSSLLGLWLLLCSCGCPEGAELRAPD KIAIIGAGIGGTS AAYYLRQKFGKDVKI
DLFEREEVGGRLATMMVQGQ EYEAGGSVIHPLNLHMKRFVKDLGLSAVQASGGLLGIYNGETL
VFEESNWFIIINVIKLVWRYGFQSLRMH MWVEDVLDKFMRIYRYQSHDYAFSSVEKLLHALGGD
DFLGMLNRTLLETLOKAGFSEKFLNEMIAPVMRVNYGQSTDINAFVGAVSLSCSDSGLWAVEG
GNKLVC SGLLQASKSNLISGSVMYIEEKT KTKYTGNPTKMYEVVYQIGTETRSDFYDIVLVAT
PLNRKMSNITFLNFDPPIEEFHQYYQHIVTTLVKGELNTSIFSSRPIDKFGLNTVLT TDNSDL
FINSIGIVPSVREKEDPEPSTDGTYVWKIFSQETLTKAQILKLFLSYDYAVKKPWLAYPHYKP
PEKCP SIIILH DRLYYLNGIECAASAMEMSAIAAHNAALLAYHRWNGHTDMIDQDGLYEKLKTEL

Important features:**Signal peptide:**

amino acids 1-23

N-glycosylation sites.

amino acids 196-200, 323-327, 353-357

Tyrosine kinase phosphorylation site.

amino acids 291-298

N-myristoylation sites.amino acids 23-29, 41-47, 43-49, 45-51, 46-52, 72-78, 115-121,
119-125, 260-266, 384-390, 459-465**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 12-23, 232-243

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FIGURE 452

MASYLYGVLFVGLCAPIYCVSPANAPSAYPRPSSTKSTPASQVYSLNTDFAFRLYRRLVLET
PSQNIFFSPVSVSTSLAMLSLGAHSVTKTQILQGLGFNLTHTPESAIHQGFQHLVHSLTVPSK
DLTLKMGSALFVKKELQLQANFLGNVKRLYEAEVFSTDFSNPSIAQARINSHVKKKTQGKVVD
IIQGLDLLTAMVLVNHIFFKAKWEKPFHLEYTRKNFPFLVGEQVTVQVPMMHQKEQFAFGVDT
ELNCFVLQMDYKGDVAFFVLPSKGMRLQEQALSARTLIKWSHSLQKRWIEVFIPRFSISAS
YNLETILPKMGIQNAFDKNADFSGIAKRDSLQVSKATHKAVLDVSEEGTEATAATTTKFIVRS
KDGPSYFTVSFNRTFLMMITNKATDGILFLGKVENPTKS

Signal peptide:
amino acids 1-20

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FIGURE 453

CTCCGGGTCCCCAGGGGCTGCGCCGGGCGGCCTGGCAAGGGGGACGAGTCAGTGGACACTCCAGGAAGAGCGGC
CCCCGGGGGGGCGATGACCGTGCGCTGACCCTGACTCACTCCAGGTCCGGAGGCGGGGGCCCCCGGGGCGACTCG
GGGGCGGACCGCGGGGCGGAGCTGCCGCCCGTGAGTCCGGCCGAGCCACCTGAGCCCCGAGCCGCGGGACACCGTC
GCTCCTGCTCTCCGAATGCTGCGCACCGCGATGGGCCTGAGGAGCTGGCTCGCCGCCCCATGGGGCGCGCTGCCG
CCTCGGCCACCGCTGCTGCTGCTCCTGCTGCTGCTGCTCCTGCTGCAGCCGCGCCTCCGACCTGGGCGCTCAGC
CCCCGGATCAGCCTGCCTCTGGGCTCTGAAGAGCGGCCATTCTCAGATTCTGAAGCTGAACACATCTCCAACTAC
ACAGCCCTTCTGCTGAGCAGGGATGGCAGGACCCTGTACGTGGGTGCTCGAGAGGCCCTCTTTGCACTCAGTAGC
AACCTCAGCTTCTGCGCAGGCGGGGAGTACCAGGAGCTGCTTTGGGGTGCAGACGCAGAGAAGAAACAGCAGTGC
AGCTTCAAGGGCAAGGACCCACAGCGCGACTGTCAAACTACATCAAGATCCTCCTGCCGCTCAGCGGCAGTCAC
CTGTTACCTGTGGCACAGCAGCCTTCAGCCCCATGTGTACCTACATCAACATGGAGAACTTCACCCTGGCAAGG
GACGAGAAGGGGAATGTCCTCCTGGAAGATGGCAAGGGCCGTTGTCCCTTCGACCCGAATTTCAAGTCCACTGCC
CTGGTGGTTGATGGCGAGCTCTACACTGGAACAGTCAGCAGCTTCCAAGGGAATGACCCGGCCATCTCGCGGAGC
CAAAGCCTTCGCCCCACCAAGACCGAGAGCTCCCTCAACTGGCTGCAAGACCCAGCTTTTGTGGCCTCAGCCTAC
ATTCTGAGAGCCTGGGCAGCTTGCAAGGCGATGATGACAAGATCTACTTTTTCTTCAGCGAGACTGGCCAGGAA
TTTGAGTTCTTTGAGAACACCATTGTGTCCCGCATTGCCCGCATCTGCAAGGGCGATGAGGGTGGAGAGCGGGTG
CTACAGCAGCGCTGGACCTCCTTCTCAAGGCCAGCTGCTGTGCTCACGGCCCGACGATGGCTTCCCCTTCAAC
GTGCTGCAGGATGTCTTCACGCTGAGCCCCAGCCCCAGGACTGGCGTGACACCCTTTTCTATGGGGTCTTCACT
TCCCAGTGGCACAGGGGAACACAGAAGGCTCTGCCGTCTGTGTCTTCACAATGAAGGATGTGCAGAGAGTCTTC
AGCGGCCTCTACAAGGAGGTGAACCGTGAGACACAGCAGTGGTACACCGTGACCCACCCGGTGCCACACCCCGG
CCTGGAGCGTGATCACCAACAGTGCCCGGGAAAGGAAGATCAACTCATCCTGCAGCTCCAGACCGCGTGCTG
AACTTCTCAAGGACCACTTCTGATGGACGGGCGAGTCCGAAGCCGCATGCTGCTGCTGCAGCCCCAGGCTCGC
TACCAGCGCGTGGCTGTACACCGCGTCCCTGGCCTGCACCACACCTACGATGTCTCTTCTGGGCACTGGTGAC
GGCCGGCTCCACAAGGCAGTGAGCGTGGGCCCCCGGTGCACATCATTGAGGAGCTGCAGATCTTCTCATCGGGA
CAGCCCGTGCAAGATCTGCTCCTGGACACCCACAGGGGGCTGCTGTATGCGGCCTCACACTCGGGCGTAGTCCAG
GTGCCCATGGCCAACTGCAGCCTGTACCGGAGCTGTGGGGACTGCCTCCTCGCCCGGGACCCCTACTGTGCTTGG
AGCGGCTCCAGCTGCAAGCAGCTCAGCCTCTACCAGCCTCAGCTGGCCACCAGGCCGTGGATCCAGGACATCGAG
GGAGCCAGCGCCAAGGACCTTTGCAGCGCGTCTTCGGTTGTGTCCCGTCTTTTGTACCAACAGGGGAGAAGCCA
TGTGAGCAAGTCCAGTTCAGCCCAACACAGTGAACACTTTGGCCTGCCCGCTCCTCTCCAACCTGGCGACCCGA
CTCTGGCTACGCAACGGGGCCCCCGTCAATGCCTCGGCCTCCTGCCACGTGCTACCCACTGGGGACCTGCTGCTG
GTGGGCACCCAAACAGCTGGGGGAGTTCCAGTGTGCTGCTACTAGAGGAGGGCTTCCAGCAGCTGGTAGCCAGCTAC
TGCCAGAGGTGGTGGAGGACGGGGTGGCAGACCAACAGATGAGGGTGGCAGTGTACCCGTATTATCAGCACA
TCGCGTGTGAGTGCACCAGCTGGTGGCAAGGCCAGCTGGGGTGCAGACAGGTCTACTGGAAGGAGTTCTTGGTG
ATGTGCACGCTCTTTGTGCTGGCCGTGCTGCTCCAGTTTTATTCTTGCTCTACCGGCACCGGAACAGCATGAAA
GTCTTCTGAAGCAGGGGGAATGTGCCAGCGTGACCCCAAGACCTGCCCTGTGGTGCTGCCCCCTGAGACCCGC
CCACTCAACGGCCTAGGGCCCCCTAGCACCCCGCTCGATCACCGAGGGTACCAGTCCCTGTGAGACAGCCCCCG
GGGGCCCGAGTCTTCACTGAGTCAGAGAAGAGGCCACTCAGCATCCAAGACAGCTTCGTGGAGGTATCCCCAGTG
TGCCCCCGGCCCGGGTCCGCCTTGGCTCGGAGATCCGTGACTCTGTGGTGTGAGAGCTGACTTCCAGAGGACGC
TGCCCTGGCTTCAGGGGCTGTGAATGCTCGGAGAGGGTCAACTGGACCTCCCCTCCGCTCTGCTCTTCGTGGAAC
ACGACCGTGGTGCCCGGCCCTTGGGAGCCTTGGAGCCAGCTGGCCTGCTGCTCTCCAGTCAAGTAGCGAAGCTCC
TACCACCCAGACACCCAAACAGCCGTGGCCCCAGAGGTCTGGCCAAATATGGGGGCTGCCTAGGTGGTGGA
CAGTGTCTCCTTATGTAACTGAGCCCTTTGTTTAAAAACAATTCCAAATGTGAACTAGAATGAGAGGGAAGAG
ATAGCATGGCATGCAGCACACACGGCTGCTCCAGTTCATGGCCTCCAGGGGTGCTGGGGATGCATCCAAAGTGG
TTGTCTGAGACAGAGTTGGAAACCCTCACCAACTGGCCTCTTACCTTCCACATTATCCCGCTGCCACCGGCTGC
CCTGTCTCACTGCAGATTGAGGACCAGCTTGGGCTGCGTGCGTTCTGCCTTGCCAGTCAGCCGAGGATGTAGTTG
TTGCTGCCGTGCTCCACACCTCAGGGACCAGAGGGCTAGGTTGGCACTGCGGCCCTCACCAGGTCTGGGCTC
GGACCCAACTCCTGGACCTTTCCAGCCTGTATCAGGCTGTGGCCACACGAGAGGACAGCGCGAGCTCAGGAGAGA
TTTCGTGACAATGTACGCCTTTCCCTCAGAATTCAGGGAAGAGACTGTGCGCTGCCTTCTCCGTTGTTGCGTGA
GAACCCGTGTGCCCTTCCCACCATATCCACCTCGCTCCATCTTTGAACTCAAACACGAGGAACCTAAGTGCACC
CTGGTCTCTCCCCAGTCCCCAGTTCACCTCCATCCCTCACCTTCTTCACTCTAAGGGATATCAACACTGCCC
AGCACAGGGGCCCTGAATTTATGTGGTTTTTATACATTTTTTAATAAGATGCACTTTATGTCATTTTTTAATAA
GTCTGAAGAATTACTGTTTAAAAA

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FIGURE 454

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA67962
><subunit 1 of 1, 837 aa, 1 stop
><MW: 92750, pI: 7.04, NX(S/T): 6
MLRTAMGLRSWLAAPWGALPPRPPLLLLLLLLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFE
AEHISNYTALLLSRDGRTLYVGAREALFALSSNLSFLPGGEYQELLWGADAEEKKQQCSFKGKD
PQRDCQNYIKILLPLSGSHLFTCGTAAFSMPCTYINMENFTLARDEKGNVLLEDGKGRCPFDP
NFKSTALVVDGELYTGTVSSFQGNPAISRSQSLRPTKTESSLNWLQDPAFVASAYIPESLGS
LQGDDDKIYFFFSETGQEFFEFFENTIVSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRPDD
GFPFNVLQDVFTLSPPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVN
RETQQWYTVTHPVPTPRPGACITNSARERKINSSLQLPDRVLFNFKDHFLMDGQVRSRMLLLQ
PQARYQRVAVHRVPGLHHTYDVLFLGTGDGRLHKAVSVGPRVHIIEELQIFSSGQPVQNLLLD
THRGLLYAASHSGVVQVPMANCSLYRSCGDCLLARDPYCAWSGSSCKHVSLEYQPQLATRPWIO
DIEGASAKDLCSASSVVSPSFVPTGEKPCQVQFQPNVTNLTACPLLSNLATRLWLRNGAPVN
ASASCHVLPTGDLLLVGTTQQLGEFQCWSLEEGFQQLVASYCPEVVEDGVADQTDEGGSPVPII
STSRVSAPAGGKASWGADRSYWKEFLVMCTLFVLAVLLPVLFLLYRHRNSMKVFLKQGECAV
HPKTCPVVLPPEPTRPLNGLGPPSTPLDHRGYQSLSDSPPGARVFTSESEKRPLSIQDSFVEVSP
VCPRPVRVLGSEIRDSVV

Transmembrane domains:

amino acids 23-46 (type II), 718-738

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FIGURE 455

TAAGATGAGGGCATCCCTCACGTTACACCCCCTGGTGGCATCTGCCAGCCCTGTTCTGGGGAC
AAGGCGGGCTTTCGTGGGAGCCATGCTCAGCCTGCCAGGAAGCCAAGCCCTACAGTGCAGAGG
AAACAGAATTTCAACGGGAAGCTGGTTTGCTTCATACCATTTGGGATCTGCTGGTAAAGCTGTT
ATTTGGGTTTAGGGACTGATCCCTTGCACTTACTTCTGGATCACCATGAATGGCCAAGATGG
TGGCAGAACACGCTGTGGACCCTGAGTTAGAGACAATGCAAATGTTGGATTGGGTGTAATTCT
TTTTGAATCCCAGATCCAGTCTGTACTTGAATATGAGCAGAAGATCTACAAGAATGCTGACAG
GGAACCGTGTTAAGACCCAGCACCCCTATTCCCAGGAGCTTCTGGCCTGACCATCTGCAGCCA
AAGCACTAACAGGGACAGATATGGGAATGTCCACCTTTGATCCGCATCCTGCACAATAGTGGT
CCCACCATGGCTGCCACTTTTTTATACTATTTGGAGAAAAGACCTTGTATAAATTCGAGGCC
GAGTGACTAACGTCTCTGTACACGGAAATGGGTAAGTGGTGGCATAGAGAAACACAATTAGC
CACTTTTTTCAGCTACACTTCTCACTCAGCTGCACCCTACACTTCTCACTCAGGTGCACCCCT
TCTGCTGTCCTTTCCCAACGTACTGGGTCCCGAGCGTGGTGGGTATTTGCCACACTGGGTGC
CAGCTCAGCAGCCCCCACCTCTCTTTATTCTCTCCAAAGCTGGTCTTTCTGACTATCATTGT
GGTAGGGGGAGGACAGATGCTAAAGGTGGAAGCTGACCTGGAGAAAGAGACACACGGGGTGAC
TGTGGCAAAGGACAGCTGGAAAAGAACTCTATCACTTCTTCATTGGCAACCACAAGGCACCC
GAGGCCATGGCACTCCAGAGGCTGTGCGCAGAGCCAAGCCTCTCAACCTCTTCTGGCCCTGC
GTCCTGCAGCGAAGTCTCTGCTGTAAGACAGTAGACTCCTTCGATGAGGTGCTCAAAAATGCT
ACCCGGGGTGGTGGTGTCTGGCTTGCACTCTGGCCCAAGTTCAGAGAAAGTTGCAGAGATCAGGG
GCCAAGGATGTCATAGCCCCAGGTTGTCCTCAGGGTCCCAATCCTAGGGCAGGGTGTGCATGG
AAGCAAGAACTATGGAAACCTAGCTCCAGTCTGCAGGCTCTGAGCCCCTAGTTCCTCACTCCA
GCGGGGCTCCCTCACTGCACAGAACCCACCCCTTCTGTGTGGGCACTGCTGACCACACAGATG
ACCCAGACCCAAAGAGCCTGGCAGAAGCTCTGTGGTTGGAGCTGGGCTCCGTCTCCAGGTCTG
GTTCAAGGGGATCAGGAAGGCTCTTTTCCACCTGTGGCTTCACTGGCCCTTTGAGATTTCTTA
TCTCACCGTTACTTCAGTTACCCTTGCAAGGGGGCCAGGGAGTCAAGAATATACCGTGTTCCTC
CAGGGTTTAAGCCGGCCATGCCTTCCCGAGAGCATAACCAACTTGACAGGGGTGCCAGTTAC
CCCACAACTGAAGGAAGGAGATCCTTCCCCCGTCCCCAGGAGTGCTCTCAACCAGCCTCAGA
AAGCTTGAGAAGATGGACCCTTTGCCCACCAGGGTTAATTCCTGGTGGGGCAGCTCGGCTGTG
ATCAGGGCAACCAAACCTATAGGAAGCCTTCCAGTGTGAGCTGGAATTAGACTGAACATGTGC
TTGGGCCTGCCTCTCCCTAGACGCAGTTGCGGGGCACTCCAGGGAATGAACCAGCTCAAGTGT
GTCCCTAACAGCAGCCTGGAGCTACCCCCAATCCCTCACAGCCTGACCCTCCTCATTCATCA
GATCTCGTGCCG

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FIGURE 456

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA69555
><subunit 1 of 1, 148 aa, 1 stop
><MW: 16214, pI: 10.22, NX(S/T): 0

MGTWWHRETQLATFSATLLTQLHPTLLTQVHPLLLSFPQRTGSRAWVVFATLGASSAAPH
LSLFSPKLVFLTIIVVGGGQMLKVEADLEKETHGVTVAKDSWKRNSITSSLATTRHPRPW
HSQRLCAEPSLSTSSGPASCSEVSAVRQ

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 64-78

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 103-107

N-myristoylation sites:

Amino acids 53-59;94-100

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FIGURE 457

CCCGCGCGCCCTGGCACTCAATCCCCGCCATGTGGGGGGCTCCTGCTCGCCCTGGCCGCCTTC
GCGCCGGCCGTCGGCCCCGGCTCTGGGGGGCGCCAGGAACCTCGGTGCTGGGCCTCGCGCAGCCC
GGGACCACCAAGGTCCCAGGCTCGACCCCGGCCCTGCATAGCAGCCCGGCACAGCCGCCGGCG
GAGACAGCTAACGGGACCTCAGAACAGCATGTCCGGATTTCGAGTCATCAAGAAGAAAAAGGTC
ATTATGAAGAAGCGGAAGAAGCTAACTCTAACTCGCCCCACCCCACTGGTGACTGCCGGGGCCC
CTTGTGACCCCCACTCCAGCAGGGACCCTCGACCCCGCTGAGAAACAAGAAACAGGCTGTCCT
CCTTTGGGTCTGGAGTCCCTGCGAGTTTCAGATAGCCGGCTTGAGGCATCCAGCAGCCAGTCC
TTTGGTCTTGGACCACACCGAGGACGGCTCAACATTCATTCAGGCCTGGAGGACGGCGATCTA
TATGATGGAGCCTGGTGTGCTGAGGAGCAGGACGCCGATCCATGGTTTCAGGTGGACGCTGGG
CACCCACCCGCTTCTCGGGTGTTATCACACAGGGGCAGGAACCTCTGTCTGGAGGTATGACTGG
GTCACATCATAACAAGGTCCAGTTCAGCAATGACAGTCGGACCTGGTGGGGAAGTAGGAACCAC
AGCAGTGGGATGGACGCAGTATTTCTGCCAATTCAGACCCAGAACTCCAGTGCTGAACCTC
CTGCCGGAGCCCCAGGTGGCCCCGCTTCATTCGCTGCTGCCCCAGACCTGGCTCCAGGGAGGC
GCGCCTTGCCCTCCGGGCAGAGATCCTGGCCTGCCCAGTCTCAGACCCCAATGACCTATTCCTT
GAGGCCCCCTGCGTCGGGATCCTCTGACCCTCTAGACTTTCAGCATCACAAATTACAAGGCCATG
AGGAAGCTGATGAAGCAGGTACAAGAGCAATGCCCAACATCACCCGCATCTACAGCATTGGG
AAGAGCTACCAGGGCCTGAAGCTGTATGTGATGGAAATGTCGGACAAGCCTGGGGAGCATGAG
CTGGGGGAGCCTGAGGTGCGCTACGTGGCTGGCATGCATGGGAACGAGGCCCTGGGGCGGGAG
TTGCTTCTGCTCCTGATGCAGTTCCTGTGCCATGAGTTCCTGCGAGGGAACCCACGGGTGACC
CGGCTGCTCTCTGAGATGCGCATTACCTGCTGCCCTCCATGAACCCTGATGGCTATGAGATC
GCCTACCACCGGGGTTTACAGAGCTGGTGGGCTGGGCGGAGGGCCGCTGGAACAACCAGAGCATC
GATCTTAACCATAATTTTGCTGACCTCAACACACCACTGTGGGAAGCACAGGACGATGGGAAG
GTGCCCCACATCGTCCCCAACCATCACCTGCCATTGCCCACTTACTACACCCTGCCCAATGCC
ACCGTGGCTCCTGAAACGCGGGCAGTAATCAAGTGGATGAAGCGGATCCCCTTTGTGCTAAGT
GCCAACCTCCACGGGGGTGAGCTCGTGGTGTCTTACCCATTCGACATGACTCGCACCCCCGTGG
GCTGCCCCGCGAGCTCACGCCCCACACAGATGATGCTGTGTTTCGCTGGCTCAGCACTGTCTAT
GCTGGCAGTAATCTGGCCATGCAGGACACCAGCCGCCGACCCTGCCACAGCCAGGACTTCTCC
GTGCACGGCAACATCATCAACGGGGCTGACTGGCACACGGTCCCCGGGAGCATGAATGACTTC
AGCTACCTACACACCAACTGCTTTGAGGTCACTGTGGAGCTGTCCTGTGACAAGTTCCCTCAC
GAGAATGAATTGCCCCAGGAGTGGGAGAACAAAGACGCCCTCCTCACCTACCTGGAGCAG
GTGCGCATGGGCATTGCAGGAGTGGTGGGGACAAGGACACGGAGCTTGGGATTGCTGACGCT
GTCATTGCCGTGGATGGGATTAACCATGACGTGACCACGGCGTGGGGCGGGGATTATTGGCGT
CTGCTGACCCCAGGGGACTACATGGTGAAGTGGCAGTGCCGAGGGCTACCATTCAGTGACACGG
AACTGTGCGGTCACCTTTGAAGAGGGGCCCTTCCCCTGCAATTTCTGTGCTCACCAAGACTCCC
AAACAGAGGCTGCGCGAGCTGCTGGCAGCTGGGGCCAAGGTGCCCCCGGACCTTCGCAGGCGC
CTGGAGCGGCTAAGGGGACAGAAGGATTGATACCTGCGGTTTAAGAGCCCTAGGGCAGGCTGG
ACCTGTCAAGACGGGAAGGGGAAGAGTAGAGAGGGAGGGACAAAGTGAGGAAAAGGTGCTCAT
TAAAGCTACCGGGCACCTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 458

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71162
><subunit 1 of 1, 734 aa, 1 stop
><MW: 81677, pI: 6.60; NX(S/T): 6
MWGLLLALAAFAVGPALGAPRNSVLGLAQPGTTKVPGSTPALHSSPAQPPAETANGTS
EQHVRIIRVIKKKKVIMKKRKKLTLTRPTPLVTAGPLVTPTPAGTLDPAEKQETGCPPLGL
ESLRVSDSRLEASSSQSFGLGPHRGRLNIHSGLEDGDLYDGAWCAEEQDADPWFQVDAGH
PTRFSGVITQGRNSVWRYDWVTSYKVQFSNDSRTWWGSRNHSSGMDAVFPANSDPETPVL
NLLPEPQVARFIRLLPQTWLQGGAPCLRAEILACPVSDPNDLFLEAPASGSSDPLDFQHH
NYKAMRKLMKQVQEQCPNITRIYSIGKSYQGLKLYVMEMSDKPGEHELGEPEVRYVAGMH
GNEALGRELLLLLMQFLCHEFLRGNPRVTRLLSEMRIHLLPSMNPDGYEIAHYHRGSELVG
WAEGRWNNQSIDLNHNFADLNTPLWEAQDDGKVPHIVPNHHLPLPTYTLPNATVAPETR
AVIKWMKRIPFVLSANLHGGELVVSYPFDMTRTPWAARELTPTPDDAVERWLSTVYAGSN
LAMQDTSRRPCHSQDFSVHGNIINGADWHTVPGSMNDFSYLHTNCFEVTVELSCDKFPHE
NELPQEWENNKDALLTYLEQVRMGIAGVVRDKDTELGIADAVIAVDGINHDVTTAWGGDY
WRLLTPGDYMVTASAEGYHSVTRNCRVTFEEGPFPCNFVLTKTPKQRLRELLAAGAKVPP
DLRRRLERLRGQKD
```

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FIGURE 459

TAAAACAGCTACAATATTCCAGGGCCAGTCACTTGCCATTTCTCATAACAGCGTCAGAGAGAA
AGAACTGACTGAAACGTTTGAGATGAAGAAAGTTCTCCTCCTGATCACAGCCATCTTGGCAGT
GGCTGTTGGTTTCCCAGTCTCTCAAGACCAGGAACGAGAAAAAAGAAGTATCAGTGACAGCGA
TGAATTAGCTTCAGGGTTTTTTGTGTTCCCTTACCCATATCCATTTGCCCCACTTCCACCAAT
TCCATTTCCAAGATTTCCATGGTTTAGACGTAATTTTCCTATTCCAATACCTGAATCTGCCCC
TACAACCTCCCCTTCCTAGCGAAAAGTAAACAAGAAGGATAAGTCACGATAAACCTGGTCACCT
GAAATTGAAATTGAGCCACTTCCTTGAAGAATCAAATTCCTGTTAATAAAAGAAAAACAAAT
GTAATTGAAATAGCACACAGCATTCTCTAGTCAATATCTTTAGTGATCTTCTTTAATAAACAT
GAAAGCAAAGATTTTGGTTTCTTAATTTCCACA

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FIGURE 460

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA71290
><subunit 1 of 1, 85 aa, 1 stop
><MW: 9700, pI: 9.55, NX(S/T): 0
MKKVLLLLITAILAVAVGFPVSQDQEREKRSISDSDELASGFFVFPYPYPRPLPPIPFPRFPW
FRRNFPIPIPIESAPTTPLPSEK

Important features of the protein:**Signal peptide:**

amino acids 1-17

Homologous region to B3-hordein:

amino acids 47-85

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-glycosylation sites:

Amino acids 57-61;210-214;220-224;318-322;428-432;472-476

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 80-84

N-myristoylation sites:Amino acids 3-9;20-29;39-48;152-161;161-170;262-271;358-364;
538-544;560-566;637-643**Zinc carboxypeptidases, zinc-binding region 2 signature:**

Amino acids 498-509

Zinc carboxypeptidases:

Amino acids 391-411

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FIGURE 461

AGCAGGAGCAGGAGAGGGACAATGGAAAGCTGCCCCGTCCAGGTTTCATGTTCCCTCTTATTTCTC
CTCACGTGTGAGCTGGCTGCAGAAGTTGCTGCAGAAGTTGAGAAATCCTCAGATGGTCCTGGT
GCTGCCCAGGAACCCACGTGGCTCACAGATGTCCCAGCTGCCATGGAATTCATTGCTGCCACT
GAGGTGGCTGTCATAGGCTTCTTCCAGGATTTAGAAATACCAGCAGTGCCCATACTCCATAGC
ATGGTGCAAAAATTCCCAGGCGTGTCAATTTGGGATCAGCACTGATTCTGAGGTTCTGACACAC
TACAACATCACTGGGAACACCATCTGCCTCTTTGCGCTGGTAGACAATGAACAACCTGAATTTA
GAGGACGAAGACATTGAAAGCATTGATGCCACCAAATTGAGCCGTTTCATTGAGATCAACAGC
CTCCACATGGTGACAGAGTACAACCCTGTGACTGTGATTGGGTTATTCAACAGCGTAATTCAG
ATTCATCTCCTCCTGATAATGAACAAGGCCTCCCCAGAGTATGAAGAGAACATGCACAGATAC
CAGAAGGCAGCCAAGCTCTTCCAGGGGAAGATTCTCTTTATTCTGGTGGACAGTGGTATGAAA
GAAAATGGGAAGGTGATATCATTTTTTCAAATAAAGGAGTCTCAACTGCCAGCTTTGGCAATT
TACCAGACTCTAGATGACGAGTGGGATACACTGCCCACAGCAGAAGTTTCCGTAGAGCATGTG
CAAACTTTTGTGATGGATTCTTAAGTGGAAAATTGTTGAAAGAAAATCGTGAATCAGAAGGA
AAGACTCCAAAGGTGGAACCTCTGACTTCTCCTTGGAACCTACATATGGCCAAGTATCTACTTTA
TGCAAAGTAAAAAGGCACAACCTCAAATCTCAGAGACACTAAACAACAGGATCACTAGGCCTGC
CAACCACACACACACGCACGTGCACACACGCACGCACGCGTGCACACACACACGCGCACACAC
ACACACACACAGAGCTTCATTTCCCTGTCTTAAATCTCGTTTTCTCTTCTTCTTCTTTTAAA
TTTCATATCCTCACTCCCTATCCAATTTCCCTTCTTATCGTGCATTCATACTCTGTAAGCCCAT
CTGTAACACACCTAGATCAAGGCTTTAAGAGACTCACTGTGATGCCTCTATGAAAGAGAGGCA
TTCCTAGAGAAAGATTGTTCCAATTTGTCATTTAATATCAAGTTTGTATACTGCACATGACTT
ACACACAACATAGTTCCTGCTCTTTTAAGGTTACCTAAGGGTTGAAACTCTACCTTCTTTTCAT
AAGCACATGTCCGTCTCTGACTCAGGATCAAAAACCAAAGGATGGTTTTAAACACCTTTGTGA
AATTGTCTTTTTTGCCAGAAGTTAAAGGCTGTCTCCAAGTCCCTGAACTCAGCAGAAATAGACC
ATGTGAAAACCTCCATGCTTGGTTAGCATCTCCAACCTCCCTATGTAAATCAACAACCTGCATAA
TAAATAAAAGGCAATCATGTTATA

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FIGURE 462

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76401

><subunit 1 of 1, 273 aa, 1 stop

><MW: 30480, pI: 4.60, NX(S/T): 1

MEAAPSRFMFLLFLLTCELAEEVAAEVEKSSDGPAAQEPTWLTDVPAAMEFIAATEVAVIGF
FQDLEIPAVPILHSMVQKFPVSGISTDSEVLTHYNITGNTICLFRLLVDNEQLNLEDEDIES
IDATKLSRFIEINSLHMTVEYNPVTVIGLFNSVIQIHLLIMNKASPEYEENMHRYQKAAKLF
QGKILFILVDSGMKENGKVISFFKLKESQLPALAIYQTLDDDEWDTLPTAEVSVEHVQNFCDF
LSGKLLKENRESEGKTPKVEL

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 143-162

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FIGURE 463

CTCGCTTCTTCCTTCTGGATGGGGGCCCAGGGGGCCCAGGAGAGTATAAAGGCGATGTGGAGG
GTGCCCCGGCACAACCAGACGCCCAGTCACAGGCGAGAGCCCTGGG**ATG**CACCGGCCAGAGGCC
ATGCTGCTGCTGCTCACGCTTGCCCTCCTGGGGGGCCCCACCTGGGCAGGGAAGATGTATGGC
CCTGGAGGAGGCAAGTATTTACGACCACTGAAGACTACGACCATGAAATCACAGGGCTGCGG
GTGTCTGTAGGTCTTCTCCTGGTGAAAAGTGTCCAGGTGAAACTTGGAGACTCCTGGGACGTG
AAACTGGGAGCCTTAGGTGGGAATACCCAGGAAGTCACCCTGCAGCCAGGCGAATACATCACA
AAAGTCTTTGTGCGCCTTCCAAGCTTTCCTCCGGGGTATGGTCATGTACACCAGCAAGGACCGC
TATTTCTATTTTGGGAAGCTTGATGGCCAGATCTCCTCTGCCTACCCCAGCCAAGAGGGGCAG
GTGCTGGTGGGCATCTATGGCCAGTATCAACTCCTTGGCATCAAGAGCATTGGCTTTGAATGG
AATTATCCACTAGAGGAGCCGACCACTGAGCCACCAGTTAATCTCACATACTCAGCAAATCA
CCCGTGGGTCGC**TAG**GGTGGGGTATGGGGCCATCCGAGCTGAGGCCATCTGTGTGGTGGTGGC
TGATGGTACTGGAGTAACTGAGTCGGGACGCTGAATCTGAATCCACCAATAAATAAAGCTTCT
GCAGAAAA

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FIGURE 464

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76541
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19600, pI: 5.89, NX(S/T): 1
MHRPEAMLLLLTLALLGGPTWAGKMYGPGGGKYFSTTEDYDHEITGLRVSVGLLLVKSQVVKL
GDSWDVKLGALGGNTQEVTLQPGYITKVFVAFQAFRLGMVMYTSKDRYFYFGKLDGQISSAY
PSQEGQVLVGIYGQYQLLGIKSIGFEWNYPLEEPTTEPPVNLTYSANSPVGR

Signal peptide:
amino acids 1-22

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FIGURE 465

CGGACGCGTGGGTCCGGCGGCCTGAGGCTGCACCGGGCACGGGTCCGGCCGCAATCCAGCCTGGGCGGAGCCGGAG
TTGCGAGCCGCTGCCTAGAGGCCGAGGAGCTCACAGCTATGGGCTGGAGGCCCGGAGAGCTCGGGGGACCCCGT
TGCTGCTGCTGCTACTACTGCTGCTGCTCTGGCCAGTGCCAGGCGCCGGGGTGCTTCAAGGACATATCCCTGGGC
AGCCAGTCACCCCGCACTGGGTCTGGATGGACAACCCTGGCGCACCGTCAGCCTGGAGGAGCCGGTCTCGAAGC
CAGACATGGGGCTGGTGGCCCTGGAGGCTGAAGGCCAGGAGCTCCTGCTTGAGCTGGAGAAGAACCACAGGCTGC
TGGCCCCAGGATACATAGAAACCCACTACGGCCCAGATGGGCAGCCAGTGGTGCTGGCCCCCAACCACACGGATC
ATTGCCACTACCAAGGGCGAGTAAGGGGCTTCCCCGACTCCTGGGTAGTCCTCTGCACCTGCTCTGGGATGAGTG
GCCTGATCACCTCAGCAGGAATGCCAGCTATTATCTGCGTCCCTGGCCACCCCGGGGCTCCAAGGACTTCTCAA
CCCACGAGATCTTTCGGATGGAGCAGCTGCTCACCTGGAAAGGAACCTGTGGCCACAGGGATCCTGGGAACAAAG
CGGGCATGACCAGCCTTCTGGTGGTCCCCAGAGCAGGGGCGAGGCGAGAAGCGCGCAGGACCCGGAAGTACCTGG
AACTGTACATTGTGGCAGACCACACCCTGTTCTTGAAGTCCGGACCGAACTTGAACCACACCAAACAGCGTCTCC
TGGAAAGTCGCCAACTACGTGGACCAGCTTCTCAGGACTCTGGACATTCAAGTGGCGCTGACCGGCTGGAGGTGT
GGACCGAGCGGGACCGCAGCCGCGTCACGCAGGACGCCAACGCCACGCTCTGGGCCTTCTGCAGTGGCGCCGGG
GGCTGTGGGCGCAGCGGCCCCACGACTCCGCGCAGCTGCTCACGGGCGCGCCTTCCAGGGCGCCACAGTGGGCC
TGGCGCCCCGTCGAGGGCATGTGCCGCGCCGAGAGCTCGGGAGGCGTGAGCACGGACCACTCGGAGCTCCCCATCG
GCGCCGACGCCACCATGGCCCATGAGATCGGCCACAGCCTCGGCCTCAGCCACGACCCCGACGGCTGCTGCGTGG
AGGCTGCGGCCGAGTCCGGAGGCTGCGTCATGGCTGCGGCCACCGGGCACCCGTTTCCGCGCGTGTTCAGCGCCT
GCAGCCGCGCCAGCTGCGCGCCTTCTTCCGCAAGGGGGGCGGCGCTTGCTCTCCAATGCCCCGGACCCCGGAC
TCCCGGTGCGCGCGGCGCTCTGCGGGAACGGCTTCGTGGAAGCGGGCGAGGAGTGTGACTGCGGCCCTGGCCAGG
AGTGCCGCGACCTCTGCTGCTTTGCTCACAAGTGTGCTGCGCCCGGGGGGCCAGTGGCGCCACGGGGACTGCT
GCGTGCGCTGCTGCTGAAGCCGGCTGGAGCGCTGTGCCGCCAGGCCATGGGTGACTGTGACCTCCCTGAGTTTTT
GCACGGGCACCTCCTCCCACTGTCCCCCAGACGTTTACCTACTGGACGGCTCACCTGTGCCAGGGGCGAGTGGCT
ACTGCTGGGATGGCGCATGTCCACGCTGGAGCAGCAGTGCCAGCAGCTCTGGGGGCTGGCTCCACCCAGCTC
CCGAGGCCTGTTTCCAGGTGGTGAAGTCTGCGGGAGATGCTCATGGAACTGCGGCCAGGACAGCGAGGGCCACT
TCCTGCCCTGTGCAGGGAGGGATGCCCTGTGTGGGAAGCTGCAGTGCCAGGGTGGAAAGCCAGCCTGCTCGCAC
CGCACATGGTGCCAGTGGACTCTACCGTTCACCTAGATGGCCAGGAAGTGAAGTGTGCGGGAGCCTTGGCACTCC
CCAGTGCCAGCTGGACCTGCTTGGCCTGGGCCTGGTAGAGCCAGGCACCCAGTGTGGACCTAGAATGGTGTGCC
AGAGCAGGCGCTGCAGGAAGAATGCCTTCCAGGAGCTTCAGCGCTGCCTGACTGCCTGCCACAGCCACGGGGTTT
GCAATAGCAACCATAACTGCCACTGTGCTCCAGGCTGGGCTCCACCCTTCTGTGACAAGCCAGGCTTTGGTGGCA
GCATGGACAGTGGCCCTGTGCAGGCTGAAAACCATGACACCTTCTGCTGGCCATGCTCCTCAGCGTCTGCTGC
CTCTGCTCCCAGGGGCGGCGCTGGCCTGGTGTGCTACCGACTCCAGGAGCCATCTGCAGCGATGCAGCTGGG
GCTGCAGAAGGGACCCCTGCGTGCAGTGGCCCCAAAGATGGCCACACAGGGACCAACCCCTGGGCGGCGTTTACC
CCATGGAGTTGGGCCCCACAGCCACTGGACAGCCCTGGCCCTGGACCCTGAGAACTCTCATGAGCCAGCAGCC
ACCCCTGAGAAGCCTCTGCCAGCAGTCTCGCTGACCCCAAGCAGATCAAGTCCAGATGCCAAGATCCTGCCTCT
GGTGAGAGGTAGCTCCTAAAATGAACAGATTTAAAGACAGGTGGCCACTGACAGCCACTCCAGGAAGTTGAACTG
CAGGGGCGAGAGCCAGTGAATCACCGGACCTCCAGCACCTGCAGGCAGCTTGGAAGTTTCTTCCCCGAGTGGAGCT
TCGACCCACCCACTCCAGGAACCCAGAGCCACATTAGAAGTTCTGAGGGCTGGAGAACACTGCTTGGGCACACT
CTCCAGCTCAATAAACCATCAGTCCCAGAAGCAAAGGTCACACAGCCCTGACCTCCCTCACCAGTGGAGGCTGG
GTAGTGCTGGCCATCCCAAAGGGCTCTGTCTGGGAGTCTGGTGTGTCTCTACATGCAATTTCCACGGACCCA
GCTCTGTGGAGGGCATGACTGCTGGCCAGAAGCTAGTGGTCTGGGGCCCTATGGTTTCTGACTGAGTCCACACTCC
CCTGCAGCCTGGCTGGCCTCTGCAAACAAACATAATTTTGGGGACCTTCTTCTCTGTTTCTTCCCACCCCTGTCTT
CTCCCCTAGGTGGTTCCTGAGCCCCCACCCTCAATCCAGTGCTACACCTGAGGTTCTGGAGCTCAGAATCTGAC
AGCCTCTCCCCATTCTGTGTGTGTCCGGGGGACAGAGGGAACCATTTAAGAAAAGATACCAAAGTAGAAGTCAA
AAGAAAGACATGTTGGCTATAGGCGTGGTGGCTCATGCCATATAATCCAGCACTTTGGGAAGCCGGGGTAGGAGG
ATCACCAGAGGCCAGCAGGTCCACACCAGCCTGGGCAACACAGCAAGACACCGCATCTACAGAAAAATTTTAAAA
TTAGCTGGGCGTGGTGGTGTGTACCTGTAGGCCTAGCTGCTCAGGAGGCTGAAGCAGGAGGATCACTTGAGCCTG
AGTTCAACACTGCAGTGAGCTATGGTGGCACCACTGCACTCCAGCCTGGGTGACAGAGCAAGACCCTGTCTCTAA
AATAAATTTTAAAAGGACTTAAAAAAGGAAAAAAGAAAAAAGAAAAAAGAAAAA

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FIGURE 466

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76788
><subunit 1 of 1, 813 aa, 1 stop
><MW: 87739, pI: 6.94, NX(S/T): 5

MGWRPRRARGTPLLLLLLLLLLLWPVPGAGVLQGHIPGQPVTPHWVLDGQPWRTVSLEEFVSKPDMGLVALEAEGQ
ELLLELEKNHRLAPGYIETHYGPDPVVLAPNHTDHCHYQGRVRFPSWVVLCTCSGMSGLITLSRNASYYL
RPWPPRGSKDFSTHEIFRMEQLLTWKGTCGHRDPGNKAGMTSLPGGPQSRGRREARRTRKYLELYIVADHTLFLT
RHRNLNHTKQRLLEVANYVDQLLRTLDIQVALTGLEWTERDRSRVTQDANATLWAFQWRRGLWAQRPHDSAQL
LTGRAFGATVGLAPVEGMCRAESSGGVSTDHSELPIGAAATMAHEIGHSLGLSHDPDGCCVEAAAESGGCVMAA
ATGHPFPRVFSACSRRLRAFFRKGGGACLSNAPDPGLPVPPALCGNGFVEAGEECDCGPGQECRDLCCFAHNCS
LRPGAQCAHGDCCVRCLLKPAGALCRQAMGDCDLPEFCTGTSSHCPPDVYLLDGSPCARGSGYCWDGACPTLEQQ
CQQLWGPGSHPAPEACFQVNSAGDAHGNCQDSEGHFLPCAGRDALCGKLCQGGKPSLLAPHMVPVDSTVHLD
GQEVTCRGALALPSAQLDLLGLGLVEPGTQCGPRMVCQSRRCRKNFQELQRCLTACHSHGVCNSNHNCHCAPGW
APPFCDKPGFGGSMDSGPVQAENHDTFLLAMLLSVLLPLLPGAGLAWCCYRLPGAHLQRCSWGCRDPACSGPKD
GPHRDHPLGGVHPMELGPTATGQPWPLDPENSHEPSSHPEKPLPAVSPDPQADQVQMPRSCLW

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domain:

Amino acids 702-720

N-glycosylation sites:

Amino acids 109-113;145-149;231-235;276-280;448-452

Tyrosine kinase phosphorylation site:

Amino acids 236-244

N-myristoylation sites:

Amino acids 29-35;185-191;195-201;308-314;318-324;326-332;338-344;370-376;
400-406;402-408;454-460;504-510;510-516;517-523;580-586;
601-607;661-667;687-693;717-723;719-725

Amidation site:

Amino acids 200-204

Neutral zinc metallopeptidases, zinc-binding region signature:

Amino acids 342-352

FIGURE 467

[illegible]

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FIGURE 468

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77623
><subunit 1 of 1, 97 aa, 1 stop
><MW: 10160, pI: 6.56, NX(S/T): 0
MQLGTGLLLAAVLSLQLAAAEAIWCHQCTGFGGCSHGSRCLRDSTHCVTTATRVLSNTEDLPL
VTKMCHIGCPDIPSLGLGPYYSIACCQTSLCNHD

Important features of the protein:

Signal peptide:

amino acids 1-20

N-myristoylation sites.

amino acids 6-11 and 33-38

Prokaryotic membrane lipoprotein lipid attachment sites.

amino acids 24-34 and 78-88

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FIGURE 469

CATGGAGCCTCTTGCAGCTTACCCGCTAAAATGTTCCGGGGCCAGAGCAAAGGTATTTGCAGT
TTTGCTGTCTATAGTTCTATGCACAGTAACGCTATTTCTTCTACAACATAAAATTCCTCAAACC
TAAAATCAACAGCTTTTATGCCTTTGAAGTGAAGGATGCAAAAGGAAGAAGTGTCTCTGGA
AAAGTATAAAGGCAAAGTTTCACTAGTTGTAAACGTGGCCAGTGACTGCCAACTCACAGACAG
AAATTACTTAGGGCTGAAGGAACTGCACAAAGAGTTTGGACCATCCCACTTCAGCGTGTTGGC
TTTTCCCTGCAATCAGTTTGGAGAATCGGAGCCCCGCCCAAGCAAGGAAGTAGAATCTTTTGC
AAGAAAAAACTACGGAGTAACTTTCCCCATCTTCCACAAGATTAAAGATTCTAGGATCTGAAGG
AGAACCTGCATTTAGATTTCTTGTTGATTCTTCAAAGAAGGAACCAAGGTGGAATTTTTTGAA
GTATCTTGTCAACCCTGAGGGTCAAGTTGTGAAGTTCTGGAGGCCAGAGGAGCCCATTGAAGT
CATCAGGCCTGACATAGCAGCTCTGGTTAGACAAGTGATCATAAAAAAGAAAGAGGATCTATGT
AGAATGCCATTGCGTTTCTAATAGAACAGAGAAATGTCTCCATGAGGGTTTGGTCTCATTTTA
AACATTTTTTTTTTTGGAGACAGTGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTAGTGCGTT
CTCAGCTCATTGCAACCTCTGCCTTTTTTAAACATGCTATTAAATGTGGCAATGAAGGATTTTT
TTTTAATGTTATCTTGCTATTAAGTGGTAATGAATGTTCCCAGGATGAGGATGTTACCCAAAG
CAAAATCAAGAGTAGCCAAAGAATCAACATGAAATATATTAATACTACTTCCTCTGACCATACT
AAAGAATTCAGAATACACAGTGACCAATGTGCCTCAATATCTTATTGTTCAACTTGACATTTT
CTAGGACTGTACTTGATGAAAATGCCAACACACTAGACCACTCTTTGGATTCAAGAGCACTGT
GTATGACTGAAATTTCTGGAATAACTGTAAATGGTTATGTTAATGGAATAAAACACAAATGTT
GAAAAATGTAAAATATATATACATAGATTCAAATCCTTATATATGTATGCTTGTTTTGTGTAC
AGGATTTTGTTTTTTCTTTTTAAGTACAGGTTCCTAGTGTTTTACTATAACTGTCACATATGTA
TGTAAGTACATATATAAATAGTCATTTATAAATGACCGTATTATAACATTTGAAAAAGTCTT
CATCAAAAAAAAAAAAAA

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FIGURE 470

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA80136

><subunit 1 of 1, 209 aa, 1 stop

><MW: 23909, pI: 9.68, NX(S/T): 0

MEPLAAYPLKCSGPRAKVFAVLLSIVLCTVTLFLLQLKFLKPKINSFYAFEVKDAKGRTVSLE
KYKGKVSLLVNVASDCQLTDRNYLGLKELHKEFGPSHFSVLAFCNQFGESEPRPSKEVESFA
RKNYGVTFPIFHKIKILGSEGEPAFRFLVDSSKKEPRWNFWKYLVNPEGQVVKFWRPEEPIEV
IRPDIAALVRQVLIKKKEDL

Important features of the protein:**Signal peptide:**

amino acids 1-31

Glutathione peroxidases signature 2.

amino acids 104-112

Glutathione peroxidases.

amino acids 57-82

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FIGURE 471

GCCCTAACCTTCCCAGGGCTCAGCTCTTTGGAGCTGCCCATTCCCTCCGGCTGCGAGAAAGGACGCGCGCCCTGCG
TCGGGCGAAGAAAAGAAGCAAACTTGTCTGGGAGGGTTTCGTTCATCAACCTCCTTCCCGCAAACCTAAACCTCCT
GCCGGGGCCATCCCTAGACAGAGGAAAGTTCCTGCAGAGCCGACCAGCCCTAGTGGATCTGGGGCAGGCAGCGGC
GCTGGCTGTGGAATTAGATCTGTTTTGAACCCAGTGGAGCGCATCGCTGGGGCTCGGAAGTCACCGTCCGCGGGC
ACCGGGTTGGCGCTGCCCAGAGTGAACCGACAGTTTGCGAGCCTCGGCTGCAAGTGGCCTCTCCTCCCCGCGGTT
GTTGTTTCAGTGTCTGGGTGAGGGCTGCGAGTGTGGCAAGTTGCAAAGAGAGCCTCAGAGGTCCGAAGAGCGCTGCG
CTCCTACTCGCGTTCGCTTCTTCTCTTCTCGGTTCCCTACTGTGAAATCGCAGCGACATTTACAAAGGCCTCCG
GGTCTACCGAGACCGATCCGACAGCGTTTGGCCCGGTCTGCTTATTCATCGGGAGCCCCGAGCACCGGCGAA
GACTGGCGGGTGGGGTAGGGAGGTGGCGGCGGCGGCATGGCGAGGTTCCCGAAGGCCGACCTGGCCGCTGCAGG
AGTTATGTTACTTTGCCACTTCTTCACGGACCAGTTTCAGTTTCGCCGATGGGAAACCCGGAGACCAAATCCTTGA
TTGGCAGTATGGAGTTACTCAGGCCTTCCCTCACACAGAGGAGGAGGTGGAAGTTGATTACACGCGTACAGCCA
CAGGTGGAAGAAACTTGGACTTTCTCAAGCGGTAGACACGAACCGAGCAAGCGTCGGCCAAGACTCTCCTGA
GCCCAGAAGCTTCACAGACCTGCTGCTGGATGATGGGCAGGACAATAACACTCAGATCGAGGAGGATACAGACCA
CAATTACTATATATCTCGAATATATGGTCCATCTGATTCTGCCAGCCGGGATTTATGGGTGAACATAGACCAAAT
GGAAAAAGATAAAGTGAAGATTCATGGAATATTGTCCAATACTCATCGGCAAGCTGCAAGAGTGAATCTGTCCTT
CGATTTTCCATTTTATGGCCACTTCTTACGTGAAATCACTGTGGCAACCGGGGGTTTCATATACACTGGAGAAGT
CGTACATCGAATGCTAACAGCCACACAGTACATAGCACCTTTAATGGCAAATTTGATCCCAGTGTATCCAGAAA
TTCAACTGTCAGATATTTTGATAATGGCACAGCACTTGTGGTCCAGTGGGACCATGTACATCTCCAGGATAATTA
TAACCTGGGAAGCTTCACATTCCAGGCAACCCTGCTCATGGATGGACGAATCATCTTTGGATACAAAGAAATTC
TGTCTTGGTCACACAGATAAGTTCAACCAATCATCCAGTGAAAGTCGGACTGTCCGATGCATTTGTCTGTGTTCCA
CAGGATCCAACAAATTTCCCAATGTTTCAAGAAGAACAATTTATGAATACCACCGAGTAGAGCTACAAATGTCAAA
AATTACCAACATTTCCGGCTGTGGAGATGACCCCATACCCACATGCCTCCAGTTTAAACAGATGTGGCCCCTGTGT
ATCTTCTCAGATTGGCTTCAACTGCAGTTGGTGTAGTAAACTTCAAAGATGTTCCAGTGGATTTGATCGTCATCG
GCAGGACTGGGTGGACAGTGGATGCCCTGAAGAGTCAAAAGAGAAGATGTGTGAGAATACAGAACCAGTGGAAAC
TTCTTCTCGAACCACCACAACCGTAGGAGCGACAACCACCCAGTTTCAGGGTCTTAACCTACCACCAGAAGAGCAGT
GACTTCTCAGTTTCCCACCAGCCTCCCTACAGAAGATGATACCAAGATAGCACTACATCTAAAAGATAATGGAGC
TTCTACAGATGACAGTGCAGCTGAGAAGAAAGGGGGAACCCCTCCACGCTGGCCTCATCATTGGAATCCTCATCCT
GGTCTTCATTGTAGCCACAGCCATTCTTGTGACAGTCTATATGTATCACCACCCAACATCAGCAGCCAGCATCTT
CTTTATTGAGAGACGCCCAAGCAGATGGCCTGCGATGAAGTTTAGAAGAGGCTCTGGACATCCTGCCTATGCTGA
AGTTGAACCAGTTGGAGAGAAAGAAGGCTTTATTGTATCAGAGCAGTGCTAAATTTCTAGGACAGAACAAACACC
AGTACTGGTTTACAGGTGTTAAGACTAAAATTTTGCTTATACCTTTAAGACAAACAAACACACACACAAAC
AAGCTCTAAGCTGCTGTAGCCTGAAGAAGACAAGATTTCTGGACAAGCTCAGCCCAGGAAACAAAGGGTAAACAA
AAAATAAACTTATACAAGATACCATTTACACTGAACATAGAATTCCTTAGTGAATGTCATCTATAGTTCACT
CGGAACATCTCCCGTGGACTTATCTGAAGTATGACAAGATTATAATGCTTTTGGCTTAGGTGCAGGGTTGCAAAG
GGATCAGAAAAAAAATCATAATAAAGCTTTAGTTCATGAGGG

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FIGURE 472

MARFPKADLAAAGVMLLCHFFTDQFQFADGKPGDQILDWQYGVTOAFPHTEEEEVEVD SHAYSH
RWKRNLDFLKAVDTN RASVGQDSPEPRSFTDLLDDGQDNNTQIEEDTDHNYYSRIYGPSDS
ASRDLWVNIDQMEKDKVKIHGILSNTHRQAARVNLSFDFPFYGHFLREITVATGGFIYTGEVV
HRMLTATQYIAPLMANFDPSVSRNSTVRYFDNGTALVVQWDHVHLQDNYNLGSFTFQATLLMD
GRIIFGYKEIPVLVTQISSSTNHPVKVGLSDAFVVVHRIQQIPNVRRRTIYEYHRVELQMSKIT
NISAVEMTPLPTCLQFNRCGPCVSSQIGFNCSWCSKLQRCSSGFDRHRQDWVDSGCPEESKEK
MCENTEPVETSSRTTTTVGATTTQFRVLTTTTRAVTSQFPTSLPTEDDTKIALHLKDNGASTD
DSAAEKKGGTLHAGLIIGILILVLIVATAILVTVMYHHPTSAASIFFIERRPSRWPAMKFERR
GSGHPAYAEVEPVGEKEGFIVSEQC

Important features of the protein:**Transmembrane domain:**

amino acids 454-478

N-glycosylation sites.

amino acids 103-107, 160-164, 213-217, 221-225, 316-320, 345-349

cAMP- and cGMP-dependent protein kinase phosphorylation sites.

amino acids 297-301, 492-496, 503-507

N-myristoylation sites.amino acids 42-48, 100-106, 147-153, 279-285, 397-403, 450-456,
455-461

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FIGURE 473

CGCGGAGCCCTGCGCTGGGAGGTGCACGGTGTGCACGCTGGACTGGACCCCCATGCAACCCCG
CGCCCTGCGCCTTAACCAGGACTGCTCCGCGCGCCCCCTGAGCCTCGGGCTCCGGCCCCGGACCT
GCAGCCTCCCAGGTGGCTGGGAAGAACTCTCCAACAATAAATACATTTGATAAGAAAGATGGC
TTTAAAAGTGCTACTAGAACAAAGAGAAAACGTTTTTCACTCTTTTAGTATTACTAGGCTATTT
GTCATGTAAAGTGACTTGTGAATCAGGAGACTGTAGACAGCAAGAATTCAGGGATCGGTCTGG
AAACTGTGTTCCCTGCAACCAGTGTGGGCCAGGCATGGAGTTGTCTAAGGAATGTGGCTTCGGC
TATGGGGAGGATGCACAGTGTGTGACGTGCCGGCTGCACAGGTTCAAGGAGGACTGGGGCTTC
CAGAAATGCAAGCCCTGTCTGGACTGCGCAGTGGTGAACCGCTTTCAGAAGGCCAAATTGTTCA
GCCACCAGTGATGCCATCTGCGGGGACTGCTTGCCAGGATTTTATAGGAAGACGAAACTTGTC
GGCTTTCAAGACATGGAGTGTGTGCCTTGTGGAGACCCTCCTCCTCCTTACGAACCGCACTGT
GCCAGCAAGGTCAACCTCGTGAAGATCGCGTCCACGGCCTCCAGCCCACGGGACACGGCGCTG
GCTGCCGTTATCTGCAGCGCTCTGGCCACCGTCCTGCTGGCCCTGCTCATCCTCTGTGTCATC
TATTGTAAGAGACAGTTTATGGAGAAGAAACCCAGCTGGTCTCTGCGGTTCGCAGGACATTCAG
TACAACGGCTCTGAGCTGTGCTGTTTTGACAGACCTCAGCTCCACGAATATGCCACACAGAGCC
TGCTGCCAGTGCCGCCGTGACTCAGTGCAGACCTGCGGGCCGGTTCGCTTGCTCCCATCCATG
TGCTGTGAGGAGGCCTGCAGCCCCAACCCGGCGACTCTTGGTTGTGGGGTGCATTCTGCAGCC
AGTCTTCAGGCAAGAAACGCAGGCCAGCCGGGGAGATGGTGCCGACTTTCTTCGGATCCCTC
ACGCAGTCCATCTGTGGCGAGTTTTTCAGATGCCTGGCCTCTGATGCAGAATCCCATGGGTGGT
GACAACATCTCTTTTTGTGACTCTTATCCTGAACTCACTGGAGAAGACATTCATTCTCTCAAT
CCAGAACTTGAAAGCTCAACGTCTTTGGATTCAAATAGCAGTCAAGATTTGGTTGGTGGGGCT
GTTCCAGTCCAGTCTCATTCTGAAAACTTTACAGCAGCTACTGATTTATCTAGATATAACAAC
ACACTGGTAGAATCAGCATCAACTCAGGATGCACTAACTATGAGAAGCCAGCTAGATCAGGAG
AGTGGCGCTGTCATCCACCCAGCCACTCAGACGTCCCTCCAGGAAGCTTAAAGAACCTGCTTC
TTTCTGCAGTAGAAGCGTGTGCTGGAACCCAAAGAGTACTCCTTTGTTAGGCTTATGGACTGA
GCAGTCTGGACCTTGCATGGCTTCTGGGGCAAAAATAAATCTGAACCAAACCTGACGGCATTTG
AAGCCTTTCAGCCAGTTGCTTCTGAGCCAGACCAGCTGTAAGCTGAAACCTCAATGAATAACA
AGAAAAGACTCCAGGCCGACTCATGATACTCTGCATCTTTCCTACATGAGAAGCTTCTCTGCCAC
AAAAGTGACTTCAAAGACTGATGGGTGAGCTGGCAGCCTATGAGATTGTGGACATATAACAA
GAAACAGAAATGCCCTCATGCTTATTTTCATGGTGATTGTGGTTTTACAAGACTGAAGACCCA
GAGTATACTTTTTCTTTCCAGAAATAATTTTCATACCGCCTATGAAATATCAGATAAATTACCT
TAGCTTTTATGTAGAATGGGTTCAAAAGTGAGTGTTTCTATTTGAGAAGGACACTTTTTTCATC
ATCTAAACTGATTCGCATAGGTGGTTAGAATGGCCCTCATATTGCCTGCCTAAATCTTGGGTT
TATTAGATGAAGTTTACTGAATCAGAGGAATCAGACAGAGGAGGATAGCTCTTTCCAGAATCC
ACACTTCTGACCTCAGCCTCGGTCTCATGAACACCCGCTGATCTCAGGAGAACACCTGGGCTA
GGGAATGTGGTCGAGAAAGGGCAGCCCATTGCCCAGAAATTAACACATATTGTAGAGACTTGTA
TGCAAAGGTTGGCATATTTATATGAAAATTAGTTGCTATAGAAACATTTGTTGCATCTGTCCC
TCTGCCTGAGCTTAGAAGGTTATAGAAAAAGGGTATTTATAAACATAAATGACCTTTTACTTG
CATTGTATCTTATACTAAAGGCTTTAGAAATTACAACATATCAGGTTCCCTACTACTGAAGT
AGCCTTCCGTGAGAACACACCACATGTTAGGACTAGAAGAAAATGCACAATTTGTAGGGGTTT
GGATGAAGCAGCTGTAACCTGCCCTAGTGTAGTTTGACCAGGACATTGTGCTGCTCCTTCCAAT
TGTGTAAGATTAGTTAGCACATCATCTCCTACTTTAGCCATCCGGTGTTGGATTTAAGAGGAC
GGTGCTTCTTTCTATTAAAGTGCTCCATCCCCTACCATCTACACATTAGCATTGTCTCTAGAG
CTAAGACAGAAATTAACCCCGTTCAGTCACAAAGCAGGGAATGGTTCATTTACTCTTAATCTT
TATGCCCTGGAGAAGACCTACTTGAACAGGGCATATTTTTTAGACTTCTGAACATCAGTATGT
TCGAGGGTACTATGATATTTTGGTTTGGAATTGCCCTGCCCAAGTCACTGTCTTTAACTTTT
AAACTGAATATTAAATGTATCTGTCTTTCCT

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FIGURE 474

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84210
><subunit 1 of 1, 417 aa, 1 stop
><MW: 45305, pI: 5.12, NX(S/T): 6
MALKVLLLEQEKTFFTLLVLLGYLSCKVTCESGDCRQQEFDRDRSGNCVPCNQCGPGMELSK
ECGFGYGEDAQCVCRLHRFKEDWGFQKCKPCLDCAVVNRFOKANCSATSDAICGDCLPG
FYRKTCLVGFQDMECVPCGDP PPPPYEPHCASKVNLVKIASTASSPRDTALAAVICSALAT
VLLALLILCVIYCKRQFMKKPSWSLSRQDIQYNGSELSCFDRPQLHEYAHRACCQCRRD
SVQTCGPVRLLPSCCEEACSPNPATLGCGVHSAASLQARNAGPAGEMVPTFFGSLTQSI
CGEFSDAWPLMQNPMGGDNISFCDSYPELTGEDIHSLNPELESSTSLDSNSSQDLVGGAV
PVQSHSENFATAATDLSRYNNTLVESASTQDALTMRSQLDQESGAVIHPATQTSLQEA

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domain:

Amino acids 169-192

N-glycosylation sites:

Amino acids 105-109;214-218;319-323;350-354;368-372;379-383

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 200-204;238-242

Tyrosine kinase phosphorylation site:

Amino acids 207-214

N-myristoylation sites:

Amino acids 55-61;215-221;270-276

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 259-270

TNFR/NGFR family cysteine-rich region proteins:

Amino acids 89-96

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FIGURE 475

AGCCAGGCAGCACATCACAGCGGGAGGAGCTGTCCCAGGTGGCCCAGCTCAGCA**ATGG**CAATG
GGGGTCCCCAGAGTCATTCTGCTCTGCCTCTTTGGGGCTGCGCTCTGCCTGACAGGGTCCCAA
GCCCTGCAGTGCTACAGCTTTGAGCACACCTACTTTGGCCCCCTTTGACCTCAGGGCCATGAAG
CTGCCCAGCATCTCCTGTCCTCATGAGTGCTTTGAGGCTATCCTGTCTCTGGACACCGGGTAT
CGCGCGCCGGTGACCCTGGTGCGGAAGGGCTGCTGGACCGGGCCTCCTGCGGGCCAGACGCAA
TCGAACCCGGACGCGCTGCCGCCAGACTACTCGGTGGTGCGCGGCTGCACAACTGACAAATGC
AACGCCCACCTCATGACTCATGACGCCCTCCCCAACCTGAGCCAAGCACCCGACCCGCCGACG
CTCAGCGGCGCCGAGTGCTACGCCTGTATCGGGGTCCACCAGGATGACTGCGCTATCGGCAGG
TCCCGACGAGTCCAGTGTCACCAGGACCAGACCGCCTGCTTCCAGGGCAGTGGCAGAATGACA
GTTGGCAATTTCTCAGTCCCTGTGTACATCAGAACCTGCCACCGGCCCTCCTGCACCACCGAG
GGCACCACCAGCCCCCTGGACAGCCATCGACCTCCAGGGCTCCTGCTGTGAGGGGTACCTCTGC
AACAGGAAATCCATGACCCAGCCCTTCACCAGTGCTTCAGCCACCACCCCTCCCCGAGCACTA
CAGGTCCTGGCCCTGCTCCTCCCAGTCCTCCTGCTGGTGGGGCTCTCAGCA**TAG**ACCGCCCCCT
CCAGGATGCTGGGGACAGGGCTCACACACCTCATTCTTGCTGCTTCAGCCCCTATCACATAGC
TCACTGGAAAATGATGTTAAAGTAAGAATTGCAAAA

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FIGURE 476

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA86576
><subunit 1 of 1, 251 aa, 1 stop
><MW: 26935, pI: 7.42, NX(S/T): 2
MAMGVPRVILLCLFGAALCLTGSQALQCYSFEHTYFGPFDLRAMKLPSISCPHECFEAILSLD
TGYRAPVTLVRKGCWTGPPAGQTQSNPDALPPDYSVVRGCTTDKCNALMLTHDALPNLSQAPD
PPTLSGAECYACIGVHQDDCAIGRSRRVQCHQDQTACFQSGRMTVGNFSVPVYIRTCHRPSC
TTEGTTSPWTAIDLQGSCEGYLCNRKSMTQPFTSASATTPPRALQVLALLLPVLLLVGLSA

Important features of the protein:**Signal peptide:**

amino acids 1-19

Transmembrane domain:

amino acids 233-251

N-glycosylation sites.

amino acids 120-124, 174-178

N-myristoylation sites.

amino acids 15-21, 84-90

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FIGURE 477

CCCACGCGTCCGGGACAGATGAACTTAAAGAGAAGCTTTAGCTGCCAAAGATTGGGAAAGGGAAAGGACAAAA
AGACCCCTGGGCTACACGGCGTAGGTGCAGGGTTTCCTACTGCTGTTCTTTTATGCTGGGAGCTGTGGCTGTAAC
CAACTAGGAAATAACGTATGCAGCAGCTATGGCTGTCAGAGAGTTGTGCTTCCCAAGACAAAGGCAAGTCCTGTT
TCTTTTTCTTTTTTGGGGAGTGTCTTGGCAGGTTCTGGGTTTGGACGTTATTCGGTGACTGAGGAAACAGAGAA
AGGATCCTTTGTGGTCAATCTGGCAAAGGATCTGGGACTAGCAGAGGGGGAGCTGGCTGCAAGGGGAACCAGGGT
GGTTTCCGATGATAACAAACAATACCTGCTCCTGGATTACATAACGGGAATTTGCTCACAAATGAGAACTGGA
CCGAGAGAAGCTGTGTGGCCCTAAAGAGCCCTGTATGCTGTATTTCCAAATTTTAATGGATGATCCCTTTCAGAT
TTACCGGGCTGAGCTGAGAGTCAGGGATATAAATGATCACGCGCCAGTATTTTCAGGACAAAGAAACAGTCTTAA
AATATCAGAAAATACAGCTGAAGGGACAGCATTTAGACTAGAAAGAGCACAGGATCCAGATGGAGGACTTAACGG
TATCCAAAACCTACACGATCAGCCCCAACTCTTTTTTCCATATTAACATTAGTGGCGGTGATGAAGGCATGATATA
TCCAGAGCTAGTGTTGGACAAAGCACTGGATCGGGAGGAGCAGGGAGAGCTCAGCTTAACCCCTCACAGCGCTGGA
TGGTGGGTCTCCATCCAGGTCTGGGACCTCTACTGTACGCATCGTTGTCTTGGACGTCAATGACAATGCCCCACA
GTTTGCCCAGGCTCTGTATGAGACCCAGGCTCCAGAAAACAGCCCCATTGGGTTCCCTTATTGTTAAGGTATGGGC
AGAAGATGTAGACTCTGGAGTCAACGCGGAAGTATCCTATTCATTTTTTGTATGCCTCAGAAAATATTTCGAACGAC
CTTTCAAATCAATCCTTTTTTCTGGGGAAATCTTCTCAGAGAATTGCTTGATTATGAGTTAGTAAATTCTTACAA
AATAAATATACAGGCAATGGACGGTGGAGGCCTTCTGCAAGATGTAGGGTTTTAGTGGAAGTATTGGACACCAA
TGACAATCCCCCTGAACTGATCGTATCATCATTTTCCAACTCTGTTGCTGAGAATTCTCCTGAGACGCCGCTGGC
TGTTTTTAAGATTAATGACAGAGACTCTGGAGAAAATGGAAAGATGGTTTTGCTACATTCAAGAGAATCTGCCATT
CCTACTAAAACCTTCTGTGGAGAATTTTACATCCTAATTACAGAAGGCGCGCTGGACAGAGAGATCAGAGCCGA
GTACAACATCACTATCACCGTCACTGACTTGGGGACACCCAGGCTGAAAACCGAGCACAACATAACGGTCCTGGT
CTCCGACGTCAATGACAACGCCCCCGCCTTCACCCAAACCTCCTACACCCCTGTTCTGTCGCGAGAACAACAGCCC
CGCCCTGCACATCGGCAGCGTCAGCGCCACAGACAGAGACTCGGGCACCAACGCCAGGTCACCTACTCGCTGCT
GCCGCCCAAGACCCGACCTGCCCTCGCCTCCCTGGTCTCCATCAACGCGGACAACGGCCACCTGTTCCGCCCT
CAGSTCGCTGGACTACGAGGCCCTGCAGGCTTTCGAGTTCGCGGTGGGCGCCACAGACCGCGGCTCCCCCGCGCT
GAGCAGAGAGGCGCTGGTGGCGGTGCTGGTGTGGACGCCAACGACAACCTCGCCCTTCGTGCTGTACCCGCTGCA
GAACGGCTCCGCGCCCTGCACCGAGCTGGTGGCCCGGGCGGCGGAGCCGGGCTACCTGGTGACCAAGSTGGTGGC
GGTGGACGGCGACTCGGGCCAGAACGCCTGGCTGTCTGTAACAGCTGCTCAAGGCCACGGAGCCCGGGCTGTTCCG
TGTGTGGGCGCACAATGGGGAGGTGCGCACCGCCAGGCTGCTGAGCGAGCGGACGACGCAAGCACAGGCTCGT
GGTGTGTTGTCAAGGACAATGGCGAGCCTCCTCGCTCGGCCACCGCCACGCTGCACTTGCTCCTGGTGGACGGCTT
CTCCCAGCCCTACCTGCCTCTCCCGGAGGCGGCCCGGCCAGGCCGAGGCCGACTTGCTCACCGTCTA
CCTGGTGGTGGCGTTGGCCTCGGTGTCTTCGCTCTTCTCCTCTCGGTGCTCCTGTTCTGTTGGCGGTGCGGCTGTG
CAGGAGGAGCAGGGCGGCCTCGGTGGGTGCTGCTCGGTGCCCGAGGGTCTTTTCCAGGGCATCTGGTGGACGT
GAGGGGCGCTGAGACCCCTGTCCAGAGCTACCAGTATGAGGTGTGTCTGACGGGAGGCCCCGGGACCAGTGAGTT
CAAGTTCTTGAAACCAGTTATTTCCGATATTACAGGCACAGGGCCCTGGGAGGAAGGGTGAAGAAAATTCACCTT
CCGAAATAGCTTTGGATTTAATATTAGTAAAGTCTGTTTTTAGTTTTCATATACTTTTGGTGTGTTACATAGCCA
TGTTTCTATTAGTTTACTTTTAAATCTCAAATTTAAGTTATTATGCAACTTCAAGCATTATTTTCAAGTAGTATA
CCCCTGTGGTTTTACAATGTTTCATCATTTTTTTTGCATTAATAACAACCTGGGTTTAATTTAATGAGTATTTTTT
CTAAATGATAGTGTTAAGGTTTTAATCTTTCCAACCTGCCCAAGGAATTAATTACTATTATATCTCATTACAGAA
ATCTGAGGTTTTGATTCATTTTCAGAGCTTGCATCTCATGATTCTAATCACTTCTGTCTATAGTGTACTTGCTCTA
TTTAAGAAGGCATATCTACATTTCCAACTCATTCTAACATTCTATATATTCGTGTTTGAAAACCATGTCATTTA
TTTCTACATCATGTATTTAAAAAGAAATATTTCTCTACTACTATGCTCATGACAAAATGAAACAAAGCATATTGT
GAGCAATACTGAACATCAATAATACCCTTAGTTTATATACTTATTATTTTATCTTTAAGCATGCTACTTTTACTT
GGCCAATATTTTCTTATGTAACTTTTGTGATGTATAAAACAGACTATGCCTTATAATTGAAATAAAATTATAA
TCTGCCTGAAATGAATAAAAATAAAACATTTTGAAATGTGAAAAAATAAAAAAAAAAAAAAAAAA

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FIGURE 478

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA87976
><subunit 1 of 1, 800 aa, 1 stop
><MW: 87621, pI: 4.77, NX(S/T): 7
MAVRELCFPRQRQVLFLFLFWGVSLAGSGFGRYSVTEETEKGSFVVNLAKDLGLAEGELAARG
TRVVSDDNKQYLLLDSTGNLLTNEKLDREKLCGPKEPCMLYFQILMDDPFQIYRAELRVRDI
NDHAPVFQDKETVLKISENTAEGTAFRLERAQDPDGGLNGIQNYTISPNSFFHINISGGDEGM
IYPELVLDKALDREEQGELSLLTALDGGSPSRSGTSTVRIVLVDVNDNAPQFAQALYETQAP
ENSPIGFLIVKVWAEDVDSGVNAEVSYSFFDASENIRTTFQINPFSGEIFLRELLDYELVNSY
KINIQAMDGGGLSARCRVLVEVLDTNDNPPELIVSSFSNSVAENSPETPLAVFKINDRDSGEN
GKMVCYIQENLPFLKPSVENFYILITEGALDREIRAEYNITITVTDLGTPLRKTEHNITVLV
SDVNDNAPAFQTQSYTLFVRENNSPALHIGSVSATDRDSGTNAQVTYSLLPPQDPHLPLASLV
SINADNGHLFALRSLDYEALQAFEFVVGATDRGSPALSREALVRVLVLDANDNSPFVLYPLQN
GSAPCTELVPRAAEPGYLVTKVAVDGDGQNAWLSYQLLKATEPGLFGVWAHNGEVRTARLL
SERDAAKHRLVVLVKDNGEPPRSATATLHLLLVLDGFSQPYLPLPEAAPAQQAQAEADLLTVYLV
VALASVSSLFLLSVLLFVAVRLCRRSRAASVGRCSVPEGPFPGHLVDVRGAETLSQSYQYEV
LTGGPGTSEFKFLKPVISDIQAQGPGRKGEENSTFRNSFGFNIQ

Important features of the protein:**Signal peptide:**

amino acids 1-26

Transmembrane domain:

amino acids 687-711

N-glycosylation sites.

amino acids 169-173, 181-185, 418-422, 436-440, 567-571, 788-792

Glycosaminoglycan attachment site.

amino acids 28-32

Tyrosine kinase phosphorylation sites.

amino acids 394-402, 578-585

N-myristoylation sites.amino acids 22-28, 27-33, 53-59, 82-88, 162-168, 184-190,
217-223, 324-330, 325-331, 471-477, 568-574, 759-765**Amidation site.**

amino acids 781-785

Aminoacyl-transfer RNA synthetases class-II signature 1.

amino acids 117-138

Cadherins extracellular repeated domain signature.

amino acids 121-132, 230-241, 335-346, 439-450, 549-560

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FIGURE 479

CTCGGCTGGATTTAAGGTTGCCGCTAGCCGCCTGGGAATTTAAGGGACCCACACTACCTTCCC
GAAGTTGAAGGCAAGCGGTGATTGTTTGTAGACGGCGCTTTGTCAATGGGACCTGTGCGGTTGG
GAATATTGCTTTTTCCTTTTTTTTGGCCGTGCACGAGGCTTGGGCTGGGATGTTGAAGGAGGAGG
ACGATGACACAGAACGCTTGCCCAGCAAATGCGAAGTGTGTAAGCTGCTGAGCACAGAGCTAC
AGGCGGAAGTGAAGTCGCACCGGTGATCTCGAGAGGTGCTGGAGCTGGGGCAGGTGCTGGATA
CAGGCAAGAGGAAGAGACACGTGCCTTACAGCGTTTCAGAGACAAGGCTGGAAGAGGCCTTAG
AGAATTTATGTGAGCGGATCCTGGACTATAGTGTTACGCTGAGCGCAAGGGCTCACTGAGAT
ATGCCAAGGGTCAGAGTCAGACCATGGCAACACTGAAAGGCCTAGTGCAGAAGGGGGTGAAGG
TGGATCTGGGGATCCCTCTGGAGCTTTGGGATGAGCCCAGCGTGGAGGTACATACCTCAAGA
AGCAGTGTGAGACCATGTTGGAGGAGTTTGAAGACATTGTGGGAGACTGGTACTTCCACCATC
AGGAGCAGCCCCTACAAAATTTTCTCTGTGAAGGTCATGTGCTCCCAGCTGCTGAAACTGCAT
GTCTACAGGAACTTGGACTGGAAAGGAGATCACAGATGGGGGAAGAGAAAACAGAAGGGGAGG
AAGAGCAGGAGGAGGAGGAGGAAGAGGAGGAAGAGGAAGGGGGAGACAAGATGACCAAGACAG
GAAGCCACCCCAAACCTTGACCGAGAAGATCTTTGACCCTTGCCCTTTGAGCCCCCAGGAGGGGA
AGGGATCATGGAGAGCCCTCTAAAGCCTGCACTCTCCCTGCTCCACAGCTTTCAGGGTGTGTT
TATGAGTGACTCCACCCAAGCTTGTAGCTGTTCTCTCCCATCTAACCTCAGGCAAGATCCTGG
TGAAACAGCATGACATGGCTTCTGGGGTGGAGGGTGGGGGTGGAGGTCCTGCTCCTAGAGATG
AACTCTATCCAGCCCCTTAATTGGCAGGTGTATGTGCTGACAGTACTGAAAGCTTTCCTCTTT
AACTGATCCCACCCCCACCCAAAAGTCAGCAGTGGCACTGGAGCTGTGGGCTTTGGGGAAGTC
ACTTAGCTCCTTAAGGTCTGTTTTTTAGACCCTTCCAAGGAAGAGGCCAGAACGGACATTCTCT
GCGATCTATATACATTGCCTGTATCCAGGAGGCTACACACCAGCAAACCGTGAAGGAGAATGG
GACACTGGGTCATGGCCTGGAGTTGCTGATAATTTAGGTGGGATAGATACTTGGTCTACTTAA
GCTCAATGTAACCCAGAGCCCACCATATAGTTTTATAGGTGCTCAACTTTCTATATCGCTATT
AACTTTTTTTCTTTTTTTCTA

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FIGURE 480

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92256
><subunit 1 of 1, 248 aa, 1 stop
><MW: 28310, pI: 4.63, NX(S/T): 0
MGPVRLGILLFLFLAVHEAWAGMLKEEDDDTERLPSKCEVCKLLSTELQAELSR TGRSREVLE
LGQVLDTGKRKRHVPYSVSETRLEEALENLCERILDYSVHAERKGSRLRYAKGQSQT MATLKGL
VQKGVKVDLGIPLELWDEPSVEVTYLKKQCETMLEEFEDIVGDWYFHHQE QPLQNFLCEGHVL
PAAETACLQETWTGKEITDGE EKTEGEEEQEEEEEEEEEGGDKMTKTGSHPKLDREDL

Important features of the protein:**Signal peptide:**

amino acids 1-21

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 106-110

N-myristoylation site.

amino acids 115-121

Amidation site.

amino acids 70-74

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FIGURE 481

GGCGTGTGCAAGGCGGGGTCCGGCCCCGCGCAGGTCGGGTAAAGCGCGTCTAGGGCGCTGCGCGG
CGCAGCGAAA**ATG**GCGGCTTCCAGGTGGGCGCGCAAGGCCGTGGTCCTGCTTTGTGCCTCTGA
CCTGCTGCTGCTGCTGCTACTGCTACCACCGCCTGGGTCTGCGCGGCCGAAGGCTCGCCCCG
GACGCCCCGACGAGTCTACCCACCTCCCCGGAAGAAGAAGGATATTCGCGATTACAATGA
TGCAGACATGGCGCGTCTTCTGGAGCAATGGGAGAAAGATGATGACATTGAAGAAGGAGATCT
TCCAGAGCACAAGAGACCTTCAGCACCTGTCGACTTCTCAAAGATAGACCCAAGCAAGCCTGA
AAGCATATTGAAAATGACGAAAAAAGGGAAGACTCTCATGATGTTTGTCACTGTATCAGGAAG
CCCTACTGAGAAGGAGACAGAGGAAATTACGAGCCTCTGGCAGGGCAGCCTTTTCAATGCCAA
CTATGACGTCCAGAGGTTTATTGTGGGATCAGACCGTGCTATCTTCATGCTTCGCGATGGGAG
CTACGCCTGGGAGATCAAGGACTTTTTGGTCCGTCAAGACAGGTGTGCTGATGTAACCTCTGGA
GGGCCAGGTGTACCCCGGCAAAGGAGGAGGAAGCAAAGAGAAAAATAAAACAAAGCAAGACAA
GGGCAAAAAAAGAAGGAAGGAGATCTGAAATCTCGGTCTTCCAAGGAAGAAAATCGAGCTGG
GAATAAAAGAGAAGACCTG**TGA**TGGGGCAGCAGTGACGCGCTGTGGGGGGACAGGTGGACGTG
GAGAGCTCTTTGCCAGCTCCTGGGGTGGGAGTGGTCTCAGGCAACTGCACACCGGATGACAT
TCTAGTGTCTTCTAGAAAGGGTCTGCCACATGACCAGTTTGTGGTCAAAGAATTACTGCTTAA
TAGGCTTCAAGTAAGAAGACAGATGTTTTCTAATTAATACTGGACACTGACAAATTCATGTTT
ACTATAAAATCTCCTTACATGGAAATGTGACTGTGTTGCTTTTTCCCATTTACACTTGGTGAG
TCATCAACTCTACTGAGATTCCACTCCCCTCCAAGCACCTGCTGTGATTGGGTGGCCTGCTCT
GATCAGATAGCAAATTCTGATCAGAGAAGACTTTAAACTCTTGACTTAATTGAGTAAACTCT
TCATGCCATATACATCATTTCATTATGTTAAAGGTAAAATATGCTTTGTGAACTCAGATGTC
TGTAGCCAGGAAGCCAGGGTGTGTAAATCCAAAATCTATGCAGGAATGCGGAGAATAGAAAA
TATGTCACTTGAAATCCTAAGTAGTTTTGAATTTCTTTGACTTGAATCTTACTCATCAGTAAG
AGAACTCTTGGTGTCTGTCAGGTTTTATGTGGTCTGTAAAGTTAGGGGTCTGTTTTGTTTCC
TTATTTAGGAAAGAGTACTGCTGGTGTGAGGGGTATATGTTCCATTTAATGTGACAGTTTT
AAAGGATTTAAGTAGGGAATCAGAGTCCTTTGCAGAGTGTGACAGACGACTCAATAACCTCAT
TTGTTTCTAAACATTTTTCTTTGATAAAGTGCCTAAATCTGTGCTTTCGTATAGAGTAACATG
ATGTGCTACTGTTGATGTCTGATTTTGCCGTTTATGTTAGAGCCTACTGTGAATAAGAGTTAG
AACATTTATATACAGATGTCATTTCTAAGAACTAAAATTCTTTGGGAAAAACCCTCAAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 482

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92289
><subunit 1 of 1, 234 aa, 1 stop
><MW: 26077, pI: 8.13, NX(S/T): 1
MAASRWARKAVVLLCASDLLLLLLLLLPPPGSCAAEGSPGTPDESTPPPRKKKKDIRDYND
ADMARLLEQWEKDDDDIEEGDLPEHKRPSAPVDFSKIDPSKPESILKMTKKGKTLMMFVTV
SGSPTEKETEEITSLWQGSLEFNANYDVQRFIVGSDRAIFMLRDGSYAWWEIKDFLVGQDRC
ADVTLEGQVYPGKGGGSKEKNKTKQDKGKKKKEGDLKSRSSKEENRAGNKREDL

Important features of the protein:**Signal peptide:**

Amino acids 1-32

N-glycosylation site:

Amino acids 201-205

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 85-89

Tyrosine kinase phosphorylation site:

Amino acids 50-59

N-myristoylation sites:

Amino acids 30-36;138-144;153-159;176-182

Amidation site:

Amino acids 207-211

FIGURE 483

[illegible]

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FIGURE 484

MALPPGPAALRHTLLLLPALLSSGWGELEPQIDGQTWAERALRENERHAFTCRVAGGPGTPRL
AWYLDGQLQEASTSRLLSVGGEAFSGGTSTFTVTAHRAQHELNCSLQDPRSGRSANASVILNV
QFKPEIAQVGAKYQEAQGPGLLVVLFALVRANPPANVTWIDQDGPVTVNTSDFLVLD AQNYPW
LTNHTVQLQLRSLAHNLSVVATNDVGVTASLPAPGPSRHPSLISSDSNNLKLNNVRLPRENM
SLPSNLQLNDLTPDSRAVKPADRQMAQNNSRPELLDPEPGGLLTSQGFIRLPVLGYIYRVSSV
SSDEIWL

N-glycosylation sites:

amino acids 106-110, 119-123, 162-166, 175-179, 192-196, 205-209,
251-255, 280-284

Glycosaminoglycan attachment site:

amino acids 23-27

Casein kinase II phosphorylation sites:

amino acids 36-40, 108-112, 164-168, 282-286, 316-320

N-myristoylation sites:

amino acids 34-40, 89-95, 215-221, 292-298, 293-299

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FIGURE 485

AGAGTTCCTTTTTCTAGGTCGATTAGGTTATACATTGTTGAAGTATAGTTTCGAGTTAGAATT
GGTCATTTTATTTTCAGTGTTTCACAGAAATCGAAGAAGACAGAAATGGCGCTTCTGTGGTGG
ATATCTACAGTAGCAATACTGTTGTTTACTTCGACGATTTTGGGAACATACGTTGAAGCTGGT
GCCGCTAAGTCTAACGAAGAAGAGATTGTGAACAAAAGCGAATTTGGAAGATTTCCACGAGGG
TCGAGAAAGGATGCATCGGGGTGCCACAAGCCGGGCTACCCTGTACCCCTCATTCTCGCTGC
CCTCCACCTCCCCATGTGCAGCGTCCTCGTCCTATTCTGCATGCTTAGTCTAACACCATCAGG
CTCGTTTATCTTTTCTGTCATTGATCTCACCAGGAGCAAATCACTAGTGCGTGCTTCTGATTC
ACGTAACGTAGTATGTAAATAAATGTCAGTGATATTATGAATTGGTAAAACATTTCTGTTATC
TAAATAAACAGTGAAGTTTGTGTTGACTAAAAAA

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FIGURE 486

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96855  
><subunit 1 of 1, 84 aa, 1 stop  
><MW: 9274, pI: 9.70, NX(S/T): 1  
MALLWWISTVAILLETSTILGTYVEAGAAKSNEEEIVNKSEFGREFPRGSRKDASGCHKPG  
YPVPPHSRCPPPPHVQRPRPILHA
```

Signal peptide:

Amino acids 1-21

N-glycosylation site:

Amino acids 38-42

N-myristoylation site:

Amino acids 27-33

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FIGURE 487

CGGGGACGGAAGCGGCCCTGGGCCCCGAGGGGCTGGAGCCGGGGCCGGGGCGATGTGGAGCGCG
GGCCGCGGCGGGGCTGCCTGGCCGGTGCTGTTGGGGCTGCTGCTGGCGCTGTTAGTGCCGGGC
GGTGGTGCCGCCAAGACCGGTGCGGAGCTCGTGACCTGCGGGTCGGTGCTGAAGCTGCTCAAT
ACGCACCACCGCGTGCGGCTGCACTCGCACGACATCAAATACGGATCCGGCAGCGGCCAGCAA
TCGGTGACCGGCGTAGAGGCGTCGGACGACGCCAATAGCTACTGGCGGATCCGCGGCGGCTCG
GAGGGCGGGTGCCCGCGCGGGTCCCCGGTGCGCTGCGGGCAGGCGGTGAGGCTCACGCATGTG
CTTACGGGCAAGAACCTGCACACGCACCACTTCCCGTCGCCGCTGTCCAACAACCAGGAGGTG
AGTGCCTTTGGGGAAGACGGCGAGGGCGACGACCTGGACCTATGGACAGTGCGCTGCTCTGGA
CAGCACTGGGAGCGTGAGGCTGCTGTGCGCTTCCAGCATGTGGGCACCTCTGTGTTCCCTGTCA
GTCACGGGTGAGCAGTATGGAAGCCCCATCCGTGGGCAGCATGAGGTCCACGGCATGCCCAGT
GCCAACACGCACAATACGTGGAAGGCCATGGAAGGCATCTTCATCAAGCCTAGTGTGGAGCCC
TCTGCAGGTCACGATGAACTCTGAGTGTGTGGATGGATGGGTGGATGGAGGGTGGCAGGTGGG
GCGTCTGCAGGGCCACTCTTGGCAGAGACTTTGGGTTTGTAGGGGTCCTCAAGTGCCTTTGTG
ATTAAAGAATGTTGGTCTATGAAA

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FIGURE 488

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96857
><subunit 1 of 1, 221 aa, 1 stop
><MW: 23598, pI: 6.96, NX(S/T): 0
MWSAGRGGAAWPVLLGLLLALLVPGGGAAGTGAELVTCGSVLKLLNTHHRVRLHSHDIKYGSG
SGQQSVTGVEASDDANSYWRIRGGSEGGCPRGSPVRCGQAVRLTHVLTGKNLHTHHFSPPLSN
NQEVSFAFGEDGE GDDLDLWTVRCSGQHWEREAAVRFQHVGT SVFLSVTGEQYGSPIRGQHEVH
GMPSANTHNTWKAMEGIFIKPSVEPSAGHDEL

Important features of the protein:**Signal peptide:**

amino acids 1-28

Glycosaminoglycan attachment site.

amino acids 62-66

N-myristoylation sites.amino acids 16-22, 25-31, 27-33, 61-67, 71-77, 86-92, 87-93,
91-97, 190-196**Endoplasmic reticulum targeting sequence.**

amino acids 218-223

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FIGURE 489

CAGCAGCCGAGACAGCAGCTGAGACGGCAGCGGCAGCTTCTCAGGGCCGGAGCCAGTTCTTGGAGGAGACTCTGC
ACAGGGCATGGATCACTGTGGTGCCCTTTTCCTGTGCCTGTGCCTTCTGACTTTGCAGAATGCAACAACAGAGAC
ATGGGAAGAACTCCTGAGCTACATGGAGAATATGCAGGTGTCCAGGGGCGGAGCTCAGTTTTTTCTCTCGTCA
ACTCCACCAGCTGGAGCAGATGCTACTGAACACCAGCTTCCAGGCTACAACCTGACCTTGCAGACACCCACCAT
CCAGTCTCTGGCCTTCAAGCTGAGCTGTGACTTCTCTGGCCTCTCGCTGACCAGTGCCACTCTGAAGCGGGTGCC
CCAGGCAGGAGGTGAGCATGCCCCGGGGTCAGCACGCCATGCAGTTCCCCGCCGAGCTGACCCGGGACGCCTGCAA
GACCCGCCCCAGGGAGCTGCGGCTCATCTGTATCTACTTCTCCAACACCCACTTTTTCAAGGATGAAAACAACCTC
ATCTCTGCTGAATAACTACGTCTTGGGGGCCAGCTGAGTCATGGGCACGTGAACAACCTCAGGGATCCTGTGAA
CATCAGCTTCTGGCACAACCAAGCCTGGAAGGCTACACCCTGACCTGTGTCTTCTGGAAGGAGGGAGCCAGGAA
ACAGCCCTGGGGGGGCTGGAGCCCTGAGGGCTGTCTGACAGAGCAGCCCTCCCACTCTCAGGTGCTCTGCCGCTG
CAACCACCTCACCTACTTTGCTGTTCTCATGCAACTCTCCCCAGCCCTGGTCCCTGCAGAGTTGCTGGCACCTCT
TACGTACATCTCCCTCGTGGGCTGCAGCATCTCCATCGTGGCCTCGCTGATCACAGTCCTGCTGCACCTTCCATTT
CAGGAAGCAGAGTGACTCCTTAACACGTATCCACATGAACCTGCATGCCTCCGTGCTGCTCCTGAACATCGCCTT
CCTGCTGAGCCCCGCATTTCGCAATGTCTCCTGTGCCCGGGTCAGCATGCACGGCTCTGGCCGCTGCCCTGCACTA
CGCGCTGCTCAGCTGCCTCACCTGGATGGCCATCGAGGGCTTCAACCTCTACCTCCTCCTCGGGCGTGTCTACAA
CATCTACATCCGCAGATATGTGTTCAAGCTTGGTGTGCTAGGCTGGGGGGCCCCAGCCCTCCTGGTGCTGCTTTC
CCTCTCTGTCAAGAGCTCGGTATACGGACCCTGCACAATCCCCGTCTTCGACAGCTGGGAGAATGGCACAGGCTT
CCAGAACATGTCCATATGCTGGGTGCGGAGCCCCGTGGTGCACAGTGTCTTGGTGCATGGGCTACGGCGGCCTCAC
GTCCCTCTTCAACCTGGTGGTGTGCTGGCCTGGGCGCTGTGGACCCTGCGCAGGCTGCGGGAGCGGGCGGATGCACC
AAGTGTGAGGGCCTGCCATGACACTGTCACTGTGCTGGGCCTCACCGTGCTGCTGGGAACCACTGGGCCTTGGC
CTTCTTTTCTTTTGGCGTCTTCTGCTGCCCCAGCTGTTCTTCTTACCATCTTAAACTCGCTGTACGGTTTCTT
CCTTTTCTGTGGTTCTGCTCCCAGCGGTGCCGCTCAGAAGCAGAGGCCAAGGCACAGATAGAGGCCTTCAGCTC
CTCCCAAACAACACAGTAGTAGTCCGGGCCTCCTGGCCTGGAATCCTCAGCCTCTCTGGCCGCCAGTAGCCTGAGGCT
ACGGCTCCTGCTAGAGAGGGGTGGCAGGCCTGCTGCTGGACCCAGAGGCCACTGTGACCGCCAAGGGGCCTTTTC
CACTTCCACGGCCTCTCCAGGCACTGAGGGGAAGGCATTGCTCTACCTCTCCCTGACATTTTGCTCCGGGGCAGA
TCCAACCTTACCTGGGGCAGCAAACCTTGTCTGTTACCTGGGGCCAGCTCGCCAGGGATGTGGGCAGAGCACCA
GCCTGGGCATCAGGAAGCCAAGTTTCAAGGACTGTCTTTGAGTCTGTCTGTATGACCTTGGGCCTGCCACTTCTC
ACAGACCCTAGGTATCCACAGCTGTGACATGGGGGCAAGCAGCTTTGTTTTCAGCCTAACCCAGGAGCTTAGTAAA
AATTGCATAAGACCAGGGGGGAAGAGTGTGAGCGTGGGGTGGGAATTCCCGCGGCCTCCACCTGCTTGCTAGGGGC
AGGATCTCATTGAGGCTGCCCTGGAAGCACCTGCTTGGCCCTGCCACCTTCTCCAGGGGAGGGCCAGATGGCAT
CCTGGCTTGGGGCGGGTGGGACCTACCCAGGCTCTGAGACTTTACTGGCCTATGCCTGAGGCCTCTTTTCTTTA
ACTCCCTAAATTATGATGACTCCAAGTCCAAGCCCACCCTTCCCAAAGATTGGGAGGTTCCGCCGTTCCAGAGG
CTCCTCCTGCGGTGCTCCCAAGACTTCCATAGACCATCTGGACCAGTAGCCCATCCCGCAGTTTTCTTGGGGGCA
GAGGAAAACGCTTCTTTCTCCTCCAGCTGAATCAGCTGGATCCAGTGTCTTGGCTGTTTGGTGATTGGGCAAGA
TTGAATTTGCCCAGGTAGGCGTGAGAGTGTGGGTTTTAAATTCGAAGCTCAGGCCATAGTTTCAGAGAATCACCC
TTACCCCAAGACCTTCATGAGACAGTGCTCATGAAGCCAGTGCGTTTCCAGAACGAACACTAGGCGGCACCGTTG
GTCCACACTCAGAGGCCCTTGGCGCCAAGACTGCATCTAGAATCGCTCAAACACCTGTTTGCAGACCCCATGCAC
CAGCTGGAGGGGCGTAACCTGCAGGACTGCGCCTACTGAGTGACCCATTTCTTCCAGGAGGAAAGGCAAGACACG
CTTACACGGCCATTTGTCTCTTTTCCCAATGCGGCGGTGCACTTTCTGCTCTTGGGGGCTGCACCCCAAGACATAGC
TGGCACCAAGAGCAGGGTGTGCTGAGGTGGTGGGTGCTCAGGGCCCTGCCCCAGGCCACTGGGCGGTTTTGATGACCT
CAAAGGTACAGGCAGAAAATAGGAGCAGGATTTCCCCTGGGGAAAAGTTATCCTGGGACATCTTCTGCTCTTCT
GTACATTTCTAGATGCAAATAACTCCTTCACCAGGCAGTGAGTGGCGTAGGCTCTGGAGCCAGGCTGCCTGGGCT
CCAATGCCAGCTCTGCCACTTGCTAGCTGTGAGACTGTGGACAAACCACTCAGCCTCTGTGTGCCTCAGTTTTCC
TATTTGTAAAATAGAGACCATAGTGGTACCTATTTTGAAGACTAAGTAAAAGAATTCAAATAAAGAGACTTGGCA
CAGAGTAAGTGCTCAGTAAAAA

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FIGURE 490

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96860
><subunit 1 of 1, 528 aa, 1 stop
><MW: 59000, pI: 8.73, NX(S/T): 9
MDHCGALFLCLCLLTQNATTETWEELLSYEMNQVSRGRSSVFSSRQLHQLEQMLLNTS
FPGYNLTLOTPTIQSLAFKLSCDFSGLSLTSATLKRVPOAGGQHARGQHMQFPAELTRD
ACKTRPRELRLICIFYFSNTHFFKDENNSSLNNYVLGAQLSHGHVNNLRDPVNISFWHNQ
SLEGYTLTCVFWKEGARKQPWGGWSPEGCRTEQPSHSQVLCRCNHLTYFAVLMQLSPALV
PAELLAPLTYISLVGCSISIVASLITVLLHFHFRKQSDSLTRIHMNLHASVLLLNI AFLL
SPAFAMSPVPGSACTALAAALHYALLSCLTWMAIEGFNLYLLLGRVYNIYIRRYVFKLGV
LGWGPALLVLLSLSVKSSVYGPCITPVFDSWENGTFQNMSCWVRSPVVHSLVMGYG
GLTSLFNLVVLAWALWTLRLRLRERADAPSVRACHDTVTVLGLTVLLGTTWALAFFSFGVF
LLPQLFLFTILNSLYGFFLFLWFCSQRCRSEAEAKAQIEAFSSSQTTQ
```

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domains:

Amino acids 244-264;290-309;316-344;358-376;411-431;468-491

N-glycosylation sites:Amino acids 18-22;58-62;65-69;146-150;147-151;173-177;
179-183;394-398;400-404**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 274-278

N-myristoylation sites:86 GLSLTS
101 GGQHAR
157 GAQLSH
255 GCSISI
311 GSACTA
420 GGLTSL
467 GTTWAL**Prokaryotic membrane lipoprotein lipid attachment sites:**

Amino acids 246-257;318-329

Eukaryotic thiol (cysteine) proteases histidine active site:

Amino acids 410-421

G-protein coupled receptors family 2 proteins:

Amino acids 273-302;314-343

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FIGURE 491

CTTGGCTGCCCCGACAACAAGCTCGCCACCTGCGCTGGGCGCATCCACCATCCAAGGCCAGCT
GAGGGGCACCAGACAGAGG**ATG**AGGAGAGAGAGTCGCACACGGGCTGCCCTGAGAGACATTTC
CATGGACATCCTCATGCTGCTTCTGCTTTTGTGTGTAATATATGGGAGATTTTCCCAAGATGA
ATACTCCCTCAATCAAGCTATCCGGAAAGAATTTACAAGAAATGCCAGAACTGCTTGGGTGG
CCTGAGAAACATCGCTGACTGGTGGGACTGGAGTCTGACCACACTTCTGGATGGCCTGTACCC
GGGAGGCACCCCGTCAGCCCGTGTGCCGGGGGCTCAGCCTGGAGCTCTTGGAGGAAAATGCTA
CCTAATAGGCAGTTCCGTAATTAGGCAGCTAAAAGTTTTTCCTAGGCATTTATGCAAGCCTCC
CAGGCCATTTTCAGCACTCATCGAAGACTCTATTCTACATGTAGTCCCGAAGTTGGAGGCC
TGAGAACCCCTACCTGATAGACCCAGAGAACC AAAACGTGACCCTGAATGGTCCTGGGGGCTG
TGGGACAAGGGAGGACTGTGTGCTCAGCCTGGGCAGAACAAAGGACTGAAGCCCACACAGCCCT
GTCCCGACTCAGGGCCAGCATGTGGATTGACCGCAGCACCAGGGCTGTGTCTGTGCACTTCAC
TCTCTATAACCCTCCAACCCAACTCTTCACCAGCGTGTCCCTGAGAGTGGAGATCCTCCCTAC
GGGGAGTCTCGTCCCTCATCCCTGGTGGAGTCATTCAGCATCTTCCGCAGCGACTCAGCCCT
GCAGTACCACCTCATGCTTCCCCAGCTGGTCTTCCTGGCACTCAGCCTGATCCACCTCTGTGT
TCAACTCTACCGTATGATGGACAAGGGCGTCCTCAGCTACTGGCGAAAGCCAAGGAACTGGCT
GGAGGTAGCCTCTCTTGTGTCATTTTCTTTTGAAAA**TAA**CAATAAACTGTTTATATCTTGAA
AAAATAATTTAAATAAGAAATTGATTATGCACTAGCTACTGCCAACATTATTGCAGTTTTCTC
CCTCTGTAGTGTTAATCTCAAAACAGCATTTGAGATCAGGTATCATTTAGTGTTGTACAGTT
ACCGTCATGTACCACACGAATTTAGCCAAAGGTGGTGGTCCCATAAGATCATATGGTGCTAAG
AAATTTCTGTCACCTAATGACATCTTGATTCTGACCTTGTATGTAGGCCTAGGCTAAATATGT
CTGTTTGTATCTTAGCTTTTAATAAAGAAGTTTAAAAATAAAAAA

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FIGURE 492

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96861
><subunit 1 of 1, 300 aa, 1 stop
><MW: 33649, pI: 9.26, NX(S/T): 1
MRRESRTAALRDISMDILMLLLLCVIYGRFSQDEYSLNQAIRKEFTRNARNCLGGLRN
IADWWDWSLTLLDGLYPGGTPSARVPGAQPGALGGKCYLIGSSVIRQLKVFPRLCKPP
RPFSAIEDSIPTCSPEVGGPENPYLIDPENQNVTLNGPGGCGTREDCVLSLGRTRTEAH
TALSRLRASMWIDRSTRAVSVHFTLYNPPTQLFTSVSLRVEILPTGSLVPSSLVESFSIF
RSDSALQYHMLLPQLVFLALSLIHLVCVQLYRMMDKGVLSYWRKPRNWLEVASLVSFSEK

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 250-267

N-glycosylation site:

Amino acids 153-157

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 2-6

N-myristoylation sites:

Amino acids 56-62;75-81;79-85;80-86;88-94;92-98;160-166

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FIGURE 493

TCTCAGGGCTTCATACAGGAAATCTATTGCTGTGTCAAGTTCCAGAGAAAAGCTTCTGTTCGT
CCAAGTTACTAACCAGGCTAAACCACATAGACGTGAAGGAAGGGGCTAGAAGGAAGGGAGTGC
CCCCTGTTGATGGGGTAAGAGGATCCTGTACTGAGAAGTTGACCAGAGAGGGTCTCACCATG
CGCACAGTTCCTTCTGTACCTGTGTGGAGGAAAAGTACTGAGTGAAGGGCAGAAAAAGAGAAA
ACAGAAATGCTCTGCCCTTGGAGAACTGCTAACCTAGGGCTACTGTTGATTTTGAATATCTTC
TTAGTGGCCGAAGCGGAGGGTGCTGCTCAACCAAACAACCTCATTAATGCTGCAAACTAGCAAG
GAGAATCATGCTTTAGCTTCAAGCAGTTTATGTATGGATGAAAAACAGATTACACAGAACTAC
TCGAAAGTACTCGCAGAAGTTAACACTTCATGGCCTGTAAAGATGGCTACAAATGCTGTGCTT
TGTTGCCCTCCTATCGCATTAAGAAATTTGATCATAATAACATGGGAAATAATCCTGAGAGGC
CAGCCTTCCTGCACAAAAGCCTACAGGAAAGAAACAAATGAGACCAAGGAAACCAACTGTACT
GATGAGAGAATAACCTGGGTCTCCAGACCTGATCAGAATTCGGACCTTCAGATTCGTCCAGTG
GCCATCACTCATGACGGGTATTACAGATGCATAATGGTAACACCTGATGGGAATTTCCATCGT
GGATATCACCTCCAAGTGTTAGTTACACCTGAACCTGACCCTGTTTCAAACAGGAATAGAAT
GCAGTATGCAAGGCAGTTGCAGGGAAGCCAGCTGCGCAGATCTCCTGGATCCCAGAGGGCGAT
TGTGCCACTAAGCAAGAATACTGGAGCAATGGCACAGTGACTGTTAAGAGTACATGCCACTGG
GAGGTCCACAATGTGTCTACCGTGACCTGCCACGTCTCCCATTTGACTGGCAACAAGAGTCTG
TACATAGAGCTACTTCCTGTTCCAGGTGCCAAAAAATCAGCAAAATTATATATTCCATATATC
ATCCTTACTATTATTATTTTGACCATCGTGGGATTCATTTGGTTGTTGAAAGTCAATGGCTGC
AGAAAATATAAATTGAATAAAACAGAATCTACTCCAGTTGTTGAGGAGGATGAAATGCAGCCC
TATGCCAGCTACACAGAGAAGAACAATCCTCTCTATGATACTACAAACAAGGTGAAGGCATCT
CAGGCATTACAAAGTGAAGTTGACACAGACCTCCATACTTTATAAGTTGTTGGACTCTAGTAC
CAAGAAACAACAACAACGAGATACATTATAATTACTGTCTGATTTTCTTACAGTTCTAGAAT
GAAGACTTATATTGAAATTAGGTTTTCCAAGGTTCTTAGAAGACATTTTAAATGGATTCTCATT
CATACCCTTGATATAATTGGAATTTTTGATTCTTAGCTGCTACCAGCTAGTTCTCTGAAGAACT
GATGTTATTACAAAGAAAATACATGCCCATGACCAAATATTCAAATTGTGCAGGACAGTAAAT
AATGAAAACCAAATTTCCCTCAAGAAATAACTGAAGAAGGAGCAAGTGTGAACAGTTTCTTGTTG
TATCCTTTCAGAATATTTTAATGTACATATGACATGTGTATATGCCTATGGTATATGTGTCAA
TTTATGTGTCCCCTTACATATACATGCACATATCTTTGTCAAGGCACCAGTGGGAACAATACA
CTGCATTACTGTTCTATACATATGAAAACCTAATAATATAAGTCTTAGAGATCATTTTATATC
ATGACAAGTAGAGCTACCTCATTCTTTTTTAATGGTTATATAAAATTCCATTGTATAGTTATAT
CATTATTTAATTAAAAACAACCCTAATGATGGATATTTAGATTCTTTTAAGTTTTGTTTATTT
CTTTTAAGTTTTGTTTGTGGTATAAACAATACCACATAGAATGTTTCTTGTTTCATATATCTCT
TTGTTTTTTGAGTATATCTGTAGGATAACTTTCTTGAGTGGAATTGTGAGGTCAAAGGGTTTGT
GCATTTTACTATTGATATATATGTTAAATTGTGTCAAATATATATGTCAAATTCCCTCCAACA
TTGTTTAAATGTGCCTTTCCCTAAATTTCTATTTTAATAACTGTACTATTCCTGCTTCTACAG
TTGCCACTTTCTCTTTTAAATCAACCAGATTAAATATGATGTGAGATTATAATAAGAATTATA
CTATTTAATAAAAAATGGATTTATA

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FIGURE 494

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96866
><subunit 1 of 1, 348 aa, 1 stop
><MW: 39069, pI: 8.13; NX(S/T): 10
MLCPWRTANLGLLLILTIFLVAEAEAGAAQPNNSLMLQTSKENHALASSSLCMDEKQITQN
YSKVLAEVNTSWPVKMATNAVLCCPPIALRNLIITWEIILRGQPSTKAYRKETNETKE
TNCTDERITWVSRPDQNSDLQIRPVAITHDGYRCIMVTPDGNFHRGYHLQVLVTPELTL
FQNRNRTAVCKAVAGKPAAQISWIPEGDCATKQEYWSNGTVTVKSTCHWEVHNVSTVTCH
VSHLTGNKSLYIELLPVPGAKKSAKLYIPYIILTIILTIIVGFIWLLKVNGCRKYKLNKT
ESTPVVEEDEMOPYASYTEKNNPLYDTTNKVKASQALQSEVDLHTL

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 78-98;267-286

N-glycosylation sites:Amino acids 31-35;60-64;69-73;116-120;122-126;185-189;
218-222;233-237;247-251;298-302**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 112-116

N-myristoylation sites:

Amino acids 103-109;259-265

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FIGURE 495

CCAGGTGCACAGCGCATCGCCCGAGGCTGTACCGCCCTGCCCCGCCCACCCCAGCTGTCCTG
GACCCAGGGGCGAGGAGAGGCTGGACGCCAGGTGCGCGGACACAGAAGCGTCTAAGCACAGCT
TCCTCCTTGCCGCTCCGGGAAGTGGGCAGCCAGCCCAGGAACCAGTACCACCTGCACCATGGG
GCTGTCCCGGAAGGAGCAGGTCTTCTTGGCCCTGCTGGGGGCTCTCGGGGGTCTCAGGCCTCAC
GGCACTCATTCTCCTCCTGGTGGAGGCCACCAGCGTGCTCCTGCCCACAGACATCAAGTTTGG
GATCGTGTTTGATGCGGGCTCCTCCCACACGTCCCTCTTCCTGTATCAGTGGCCGGCGAACAA
GGAGAATGGCACGGGTGTGGTCAGCCAGGCCCTGGCCTGCCAGGTGGAAGGGCCTGGAATCTC
CTCCTACACTTCTAATGCTGCACAGGCTGGTGAGAGCCTGCAGGGCTGCTTGGAGGAGGCGCT
GGTGCTGATCCCAGAGGCCCAGCATCGGAAAACACCCACGTTCCCTGGGGGGCCACGGCTGGCAT
GAGGTTGCTCAGCCGGAAGAACAGCTCTCAGGCCAGGGACATCTTTGCAGCAGTCACCCAGGT
CCTGGGGCCGGTCTCCCGTGGACTTTTGGGGTGCCGAGCTCCTGGCCGGGCAGGCCGAAGGTGC
CTTTGGTTGGATCACTGTCAACTACGGCTTGGGGACGCTGGTCAAGTACTCCTTCACTGGAGA
ATGGATCCAGCCTCCGGAGGAGATGCTGGTGGGTGCCCTGGACATGGGAGGGGGCCTCCACCCA
GATCACGTTGCTGCCCTGGGGGCCCCATCTTGGACAAGAGCACCCAGGCCGATTTTCGCCTCTA
CGGCTCCGACTACAGCGTCTACACTCACAGCTACCTGTGCTTTGGACGGGACCAGATGCTGAG
CAGGCTCCTCGTGGGGCTGGTGCAGAGCCGCCCGGCTGCCCTGCTCCGTCACCCGTGCTACCT
CAGCGGCTACCAGACCACACTGGCCCTGGGCCCGCTGTATGAGTCACCCTGTGTCCACGCCAC
GCCCCCGCTGAGCCTCCCCCAGAACCTCACAGTTGAAGGGACAGGCAACCCTGGAGCCTGCGT
CTCAGCCATCCGGGAACTTTCAACTTCTCCAGCTGCCAGGGCCAGGAGGACTGCGCCTTTGA
CGGGGTCTACCAGCCCCCGCTGCGGGGCCAGTTCTATGTGGAGGCCAGCTACCCTGGGCAGGA
CCGCTGGCTGCGGGACTACTGTGCCTCAGGCCTGTACATCCTCACCCTCCTGCACGAGGGCTAC
GGGTTCAGCGAGGAGACCTGGCCCAGCCTCGAGTTCCGAAAGCAGGCGGGCGGTGTGGACATT
GGCTGGACACTGGGCTACATGCTGAACCTGACCGGGATGATCCCGGCCGATGCGCCGGCTCAG
TGGCGGGCAGAGAGCTACGGCGTCTGGGTGGCCAAAGTGGTGTTCATGGTGCTGGCCCTGGTG
GCGGTGGTGGGGGCTGCCTTGGTCCAGCTCTTCTGGTTGCAGGACTAGTGGGAAGGCGGAGGT
GGGCCCCACAGAGCCCACAGGCAGCTGCGTCCCGGATGCTGGAGGCTTCTGAGCCCTGAGC
GCCGTGGGGCCTTGCTCTGTGGCTCTGCCCACGGTCAGGTGACAGCCACCTCCAGGGCACCGT
CAGGGTGGTGCTGGCCACAGAGGCTGCATGACCTCCCCTCCCGGCGTCCCTCCCCAACCTCC
TTCCGCAACTGGGCTTCCAGGGCCGCTAGGTGCCTTTCTGCACACAGGCCGCCAGGACTCGTGG
TGTCTCCAGGCTGTGTGACTGCAGGGCCACATGCTGCCTGCAAACAGGGCAAGACCACGGAGG
CACAGGGGTCTGCTCCTGATGGGGCCTCAGGAGGGGCGGAGAGGGGTGGAAGGGAGGGAGCT
GCCCCACCTGGACCCCCGCTCTCCCTGCTGTTGTCTGAGCAGATGGATGGAGTCCAGGCCTGG
GGGCTTCTGCTGGGCCAGCCCGGCTCCACACCCACTTGGAGGGTGAGACTGCAGTGGGGGT
TGTTTTTATTAAAAGCATCATGGACACAGCAAAAAAAAAAAAAAAAAA

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FIGURE 496

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96870
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49377, pI: 4.98, NX(S/T): 5
MGLSRKEQVFLALLGASGVSGLTALILLVLEATSVLLPTDIKFGIVFDAGSSHTSLFLYQ
WPANKENGTVVVSQALACQVEGPGISSYTSNAAQAGESLQGCLEEALVLIPEAQHRKTPT
FLGATAGMRLLSRKNSSQARDIFAAVTQVLGRSPVDFWGAELLAGQAEGAFGWITVNYGL
GTLVKYSFTGEWIQPPEEMLVGALDMGGASTQITFVPGGPILDKSTQADFRLYGSDYSVY
THSYLCFGRDQMLSRLLVGLVQSRPAALLRHPCYLSGYQTTLALGPLYESPCVHATPPLS
LPQNLTVEGTGNPGACVSAIRELFNFSSCQGQEDCAFDGVYQPPLRGQFYVEASYPGQDR
WLRDYCASGLYILTLLHEGYGFSEETWPSLEFRKQAGGVDIGWTLGYMLNLTGMI PADAP
AQWRAESYGVVAKVVFVVLALVAVVGAALVQLFWLQD

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 428-449

N-glycosylation sites:

Amino acids 67-71;135-139;304-308;325-329;410-414

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 133-137

N-myristoylation sites:Amino acids 50-56;123-127;165-171;207-213;234-240;
259-265;311-317;314-320;331-337;398-404;
413-419;429-435**GDA1/CD39 family of nucleoside phosphatases proteins:**

Amino acids 43-59;202-215

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FIGURE 497

GCCTTATAAAGTAGCCTCTGCATCTGCCTGCCTCGGGCAGAGGAGGGCTACCCTGGGGCTGAG
AGTTCACCTGTCTCAGGAACCACCTGAGCCCACAGATCCTGTGGGCAGCGGCCAGGGCAGCCA
TGGCTTGGGCAAGTAGGCTGGGCCTGCTGCTGGCACTGCTGCTGCCCCGTGGTCGGTGCCTCCA
CGCCAGGCACCGTGGTCCGACTCAACAAGGCAGCATTGAGCTACGTGTCTGAAATTGGGAAAG
CCCCCTCTCCAGCGGGCCCTGCAGGTCACCTGTCCCTCATTTCCCTGGACTGGAGTGGAGAGGCGC
TTCAGCCCACCAGGATCCGGATTCTGAATGTCCATGTGCCCCGCCTCCACCTGAAATTCATTG
CTGGTTTCGGAGTGCGCCTGCTGGCAGCAGCTAATTTTACTTTCAAGGTCTTTCGCGCCCCAG
AGCCCCCTGGAGCTGACGCTGCCTGTGGAAGTGTGGCTGACACCCGCGTGACCCAGAGCTCCA
TCAGGACCCCTGTGGTCAGCATCTCTGCCTGCTCTTTATTCTCGGGCCACGCCAACGAGTTTG
ATGGCAGTAACAGCACCTCCACGCGCTGCTGGTCCTGGTGCAGAAGCACATTAAAGCTGTCT
TGAGTAACAAGCTGTGCCTGAGCATCTCCAACCTGGTGCAGGGTGTCAATGTCCACCTGGGCA
CCTTAATTGGCCTCAACCCCGTGGGTCTGAGTCCCAGATCCGCTATTCATGGTCAGTGTGC
CCACTGTCACCAGTGACTACATTTCCCTGGAAGTCAATGCTGTTCTCTTCCCTGCTGGGCAACC
CCATCATCCTGCCCCACGGATGCCACCCCTTTTGTGTTGCCAAGGCATGTGGGTACCGAGGGCT
CCATGGCCACCGTGGGCCTCTCCCAGCAGCTGTTTGACTCTGCGCTCCTGCTGCTGCAGAAGG
CCGGTGGCCTCAACCTGGACATCACAGGGCAGCTGAGGTGCGATGACAACCTGCTGAACACCT
CTGCTCTGGGCGGCTCATCCCGGAGGTGGCCCGCCAGTTTCCCGAGCCCATGCCTGTGGTGC
TCAAGGTGCGGCTGGGTGCCACACCTGTGGCCATGCTCCACACAAACAACGCCACCCTGCGGC
TGCAGCCCTTCGTGGAGGTCTGGCCACAGCCTCCAACCTCGGCTTTCCAGTCCCTCTTCTCCC
TGGATGTGGTAGTGAACCTGAGACTCCAGCTCTCTGTGTCCAAGGTGAAGCTTCAGGGGACCA
CGTCTGTGCTGGGGGATGTCCAGCTCACGGTGGCCTCCTCCAACGTGGGCTTCATTGATACAGAT
CAGGTGCGCACACTGATGGGCACCGTTTTTGGAGAAGCCCCTGCTGGACCATCTCAATGCTCTC
TTGGCCATGGGAATTGCCCTCCCTGGTGTGGTCAACCTCCACTATGTTGCCCTGAGATCTTT
GTCTATGAGGGCTACGTGGTGATATCCAGTGGACTCTTCTACCAGAGCT**TGAGGCAAGACCACT**
GGGAGGCCTGAGAGTGGGCCAGCTCGCTGCTCAGGCGAATTTCTCATTTCAAGCCACTGGGGA
AACTGAGGCAAAACCATACTTAGTCATCACCAACAAGCTGGACTGCTTAGCTGGGCTGTTTTA
TCTTCCCTGAGTGCCCTGGGTCTCCCTCCCTCACTTCTGCCCTTTCCCTTCCTCCTCCTCTTCT
CCTCCCTCTTCCCTCATCTCCCCCTCCTTCCTCTGCCCCACCCAGGGGGGAGCAGACTGCT
CCTCCAGGCTGTATAGACCTGCCCTCTTGCAATTAAACAACCTTCTCTTGAGCTGC

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FIGURE 498

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96872
><subunit 1 of 1, 458 aa, 1 stop
><MW: 49158, pI: 8.72, NX(S/T): 4
MAWASRLGLLLALLLPVVGASTPGTVVRLNKAALSYVSEIGKAPLQRALQVTVPHFLDWS
GEALQPTRIRILNVHVPRLHLKFIAGFGVRLAANFTFKVFRAPEPLELTPVELLADT
RVTQSSIRTPVVSISACSLFSGHANEFDGSNSTSHALLVLVQKHIKAVLSNKLCLISISNL
VQGVNVHLGTLIGLNPVGPESQIRYSMVSVPTVTS DYISLEVNAVLFLLGNPIILPTDAT
PFVLPRHVGTEGSMATVGLSQQLFDSALLLLQKAGALNLDITGQLRSDDNLLNTSALGRL
IPEVARQFPEPMPVVLKVRLGATPVAMLHTNNATLRLQPFVEVLATASNSAFQSLFSLDV
VVNLRLQLSVSKVKLQGTTSVLGDVQLTVASSNVGFIDTDQVRTLMGTVFEEKPLLDHLNA
LLAMGIALPGVVNLHYVAPEIFVYEGYVVVISSGLFYQS

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 217-236

N-glycosylation sites:

Amino acids 96-100;151-155;293-297;332-336

N-myristoylation sites:

Amino acids 8-14;149-155;189-195;249-255;252-258;283-289

LBP / BPI / CETP family proteins:

Amino acids 22-50; 251-287

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FIGURE 499

TTGAAAATCTACTCTATCAGCTGCTGTGGTTGCCACCATTCTCAGGACCCTCGCCATGAAGC
CCTTATGCTGCTCACCCCTGTCTGTTCTGCTCTGCTGGGTCTCAGCTGACATTCGCTGTCACTC
CTGCTACAAGGTCCCTGTGCTGGGCTGTGTGGACCGGCAGTCCTGCCGCCTGGAGCCAGGACA
GCAATGCCTGACAACACATGCATACCTTGGTAAGATGTGGGTTTTCTCCAATCTGCGCTGTGG
CACACCAGAAGAGCCCTGTCAGGAGGCCTTCAACCA^{AA}ACCAACCGCAAGCTGGGTCTGACATA
TAACACCACCTGCTGCAACAAGGACAACCTGCAACAGCGCAGGACCCCGGCCCACTCCAGCCCT
GGGCCTTGTCTTCCTTACCTCCTTGGCTGGCCTTGGCCTCTGGCTGCTGCACTGAGACTCATT
CCATTGGCTGCCCCCTCCTCCCACCTGCCTTGGCCTGAGCCTCTCTCCCTGTGTCTCTGTATCC
CCTGGCTTTACAGAATCGTCTCTCCCTAGCTCCCATTCTTTAATTAAACACTGTTCCGAGTG
GTCTCCTCATCCATCCTTCCCACCTCACACCCTTCACTCTCCTTTTTCTGGGTCCCTTCCCAC
TTCCTTCCAGGACCTCCATTGGCTCCTAGAAGGGCTCCCCACTTTGCTTCCTATACTCTGCTG
TCCCCTACTTGAGGAGGGATTGGGATCTGGGCCTGAAATGGGGCTTCTGTGTTGTCCCCAGTG
AAGGCTCCCACAAGGACCTGATGACCTCACTGTACAGAGCTGACTCCCCAAACCCAGGCTCCC
ATATGTACCCCATCCCCCATACTCACCTCTTCCATTTTGAGTAATAAATGTCTGAGTCTGGA
AAAAAAAAAAAAAAAAAAAA

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FIGURE 500

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96878
><subunit 1 of 1, 125 aa, 1 stop
><MW: 13821, pI: 8.60, NX(S/T): 2
MKALMLLTLSVLLCWVSADIRCHSCYKVPVLGCVDRQSCRLEPGQQCLTTHAYLGKMWVFSNL
RCGTPEEPCQEAFNQTNRKLGLTYNTTCCNKDNCNSAGPRPTPALGLVFLTSLAGLGLWLLH

Important features of the protein:**Signal peptide:**

amino acids 1-18

N-glycosylation sites.

amino acids 77-81, 88-92

N-myristoylation site.

amino acids 84-90

Ly-6 / u-PAR domain protein signature.

amino acids 85-98

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FIGURE 501

GGAGCCTCCTAATGCAGTCTTCTGCACAGTCCTGGGGACTGACTGACTGAATCACACCTCTGG
GGCTGGGGGCTGCTGACATGTGTGCCTTTCCTTGGCTGCTTCTTCTCCTGCTGCTCCAGGAGG
GCAGCCAAAGGAGACTCTGGAGATGGTGTGGATCCGAGGAAGTGGTTGCGGTCCTTCAGGAGT
CCATCAGCCTCCCCCTGGAAATACCACCAGATGAAGAGGTTGAGAACATCATCTGGTCCTCTCAC
AAAAGTCTTGCCACTGTGGTGCCAGGGAAAGAGGGACATCCAGCTACCATCATGGTGACCAAT
CCACACTACCAGGGCCAAGTGAGCTTCCTGGACCCCAGCTATTCCCTGCATATCAGCAATCTG
AGCTGGGAGGATTCAGGGCTTTACCAAGCTCAAGTCAACCTGAGAACATCCCAGATCTCTACC
ATGCAGCAGTACAATCTATGTGTCTACCATCCTAACTATGCTTCTGAGAAGCCTTCAACAGCC
TTCTGCCTCCTGGCCAAGGGATTGCTCATCTTCTTGCTCTTGGTAATTCTGGCCATGGGACTC
TGGGTCATCCGAGTCCAGAAAAGACACAAAATGCCAAGGATGAAGAAACTCATGAGAAACAGA
ATGAAATTGAGGAAGGAGGCAAAGCCTGGCTCCAGCCCTGCCTGACTGCTCCTTGGGAACCCC
AGTCCTGAGCTTGGTTTCTTCCCAGCACCCAGAGAATCCTTCCTCAGCTCTCTTCTTCCAGG
GGAAGGAGGTGCTCAGGGGTGGGTATCCAGAGAGCCATACTTCTGAGGGAAGACTGGCTGGCA
ATAAAGTCAAATTAAGTGACCACA

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FIGURE 502

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96879
><subunit 1 of 1, 198 aa, 1 stop
><MW: 22584, pI: 9.40, NX(S/T): 1
MCAFPWLLLLLLLLQEGSQRRRLWRWCGSEEVVAVLQESISLPLEIPPDEEVENIIWSSHKS
LATVVPKGEGHPATIMVTNPHYQGQVSEFLDPSYSLHISNLSWEDSGLYQAQVNLRTSQIS
TMQQYNLCVYHPNYASEKPPSTAFCLLAKGLLIFLLLVLAMGLWVIRVQKRHKMPRMKKL
MRNRMKLRKEAKPGSSPA

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 144-165

N-glycosylation site:

Amino acids 99-103

N-myristoylation site:

Amino acids 106-112

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FIGURE 503

ACGGGCCGCGAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCAG
TCGGGCCGTTCCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCTAC
CGCACCCAGGTTTCGGCCCCGTAGGCGTCTGGCAGCCCCGGCGCCATCTTCATCGAGCGCC**ATGGC**
CGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCAATTTGTTTCTGCT
GACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTAAAAGC
TCTTACCCTCCACTATGACCGCTATAACCACCTCCCGCAGGCTGGATCCCATCCCACAGTTGAA
ATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAGTCATACAGTGTCAGAACAA
AGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCATACAAATT
TGGAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGTACTAAGAGG
TTCTTGTGGCTTGAGGTATAATTTAGATTATACAGAACTTGGCCTGCAGAACTGAAGGAGTC
TGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCCTCGGCGGATTC
CTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTTTGTAGTCTATAA
GCTGTTCCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATCCTCCATTTTCCCA
CCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTTAAGTCTGAGTTCAC
AGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGCTTTTACAGGACAACA
AGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTGGTGGAATACTAGGATA
TTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGGTACTACCCGTCCTATCC
TCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCATGGAGGCTCGGGCAGCTA
TTCGGTATGTTCAAACCTCAGACACGAAAACCAGAACTGCATCAGGATATGGTGGTACCAGGAG
ACGAT**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAATTTTGGATTTTTCATCACTTT
CTCTTTAGAAAAAAGTACTACCTGTAAACAATTGGGAAAAGGGGATATTCAAAGTTCTGTG
GTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAGGCTAAAAGTTGATGTGTGACAA
AATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTATATTGCAGTTTTTGAAAGTGATC
ATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAACCTGTGATGCCCTAAGAAGCATTA
GAATGAAGGTGTTGTACTAATAGAACTAAGTACAGAAAATTTCAAGTTTTAGGTGGTTGTAGC
TGATGAGTTATTACCTCATAGAGACTATAATATTCTATTTGGTATTATATTATTGATGTTTG
CTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAATTATGCTAATTTGTGAGTTCTGATCAC
TTTTGAGCTCTGAAGCTTTGAATCATTCAAGTGGTGGAGATGGCCTTCTGGTAACTGAATATTA
CCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTAGAAGGTGTTGTGAATGACTCTGTGCTGG
CAAAAATGCTTGAAACCTCTATATTTCTTTTCGTTTATAAGAGGTAAAGGTCAAATTTTTCAAC
AAAAGTCTTTTAATAACAAAAGCATGCAGTTCTCTGTGAAATCTCAAATATTGTTGTAATAGT
CTGTTTCAATCTTAAAAAGAATCA

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FIGURE 504

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDPIPO
LKCVGGTAGCDSYTPKVIQCQNKGWGDYDVQWECKTDLDIAYKFGKTVVSCEGYESSEDQYVL
RGSCGLEYNLDYTELGLOKLKESGKQHGFASFSDYYYKWSSADSCNMSGELITIVVLLGIAFVV
YKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGHGATSGFGSAFTG
QQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSPYPPSYPGTWNRAYSPHGGSG
SYSVCSNSDTKTRTASGYGGTRRR

Signal peptide:
amino acids 1-30

Transmembrane domain:
amino acids 171-190

N-glycosylation site.
amino acids 172-176

Glycosaminoglycan attachment sites.
amino acids 244-248, 259-263, 331-335

Tyrosine kinase phosphorylation site.
amino acids 98-106

N-myristoylation sites.
amino acids 68-74, 69-75, 131-137, 241-247, 247-253, 266-272,
270-276, 278-284, 312-318

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FIGURE 505

GCAAAAGGAAGGGAGGGAAGCACTCCATCATCTCACTGGGAAGAACGGGCACGGGCATACCTGC
AGCTACTGGGGTTCCACTGGGCTTGAGGGTCGATTTTTTCACCTTTTGAAGGACAAGATGCATT
GGAAGATGTTGCTGCTTCTGCTGTTGTATTACAATGCTGAGGCTTCTATGTGCCACAGGTGGA
GCAGGGCTGTGCTCTTCCCTGCCGCCACCGGCCAAAGAGGTCCTCATCACTGCCATTGAACC
CAGTCCTGCAGACCTCCCTGGAGGAGGTGGAGCTGCTCTACGAGTTCCTGCTGGCCGAACTTG
AGATCAGCCCTGACCTGCAGATCTCCATCAAGGACGAGGAGCTGGCCTCCTTGCGGAAGGCCT
CAGACTTCCGCACCGTCTGCAACAACGTCATCCCCAAGAGCATCCCAGACATCCGCCGGCTCA
GCGCCAGCCTCTCCAGCCACCCTGGCATCCTCAAGAAAGAAGACTTTGAAAGGACAGTGCTGA
CCCTGGCCTACACAGCCTACCGCACAGCCCTGTCCCACGGCCATCAGAAGGACATCTGGGCGC
AGTCCCTCGTTAGCCTCTTCCAGGCCCTGAGGCACGACTTGATGCGCTCCTCACAGCCGGGAG
TACCTCCCTTGAGAGACTGGCCACACCAGGACCTCAGAGCAGGGACCAGCACAGTAATCCAGA
AAGTCTTCATTCTCTACTCCATTTACAGAGACCAGCAACAAAACACTTACCGCTGACACAGAG
CAGCAGAGATCAAACAGTAACCCCGATGCTCTTTTCTCCTTGTAGTTTCCTGGAAGACACATC
TGATTCATGCCATCATGTGACCTGGGCTGGAAGAAAGGGCTGGAATGGTCATTCAAGACGCCT
CCATGGGCAGAATGGTTTGCCTATGGCAGGCAGAATTCTGATATGCTTCAACCCAGAGCAGTG
GCCACACACTCAAGAGTGAGAACAGGGCGTGAGCCACCGTGCCCTGGCCCAGGATCTAAAACTT
TCTAAGTTTCCTCCATCGTTGGCATCCTCACAGCTATCTCCAATGTCACTCAAGAGACATCAA
CAGACATTTAACTGCTGCAGACTTCATTGCTCTGTCACCTCACCTTGAATCTAACAAATCAA
GTATTTCTGCAGGTCCAATGGTCTAAAATCAAATGCTTGTTAAATGACTTTTTTACAACACCCCTT
ACTTTCCTAATCCATTTCAATCTTATTTTTTTTTATTGTGGTAAAAACACATCACGTAAATG
TACCATCTTAACCATTTTTTAAGCATATGGTACAGCAGTGTTAACTCCATGCATGTTGTGAAAC
AGACCCCCGGAACCTTCTCATCTTGTAATTCTGAAGTTCTATACCCACCGAACAACCTCCTCTT
TTCCCTTCCCCCTGCCTGCCCCAGCTCTTGGCACCATTATTCTGCTTTCTGTTTTTGAGAGT
CTGACTACTTAAGATACCTCATAAAGCGGGATCTGGCTTACATTTCTTGAGCATTTGTATTCT
GGAAAAGTGTTTCCTTCCTCTGAAAAATGGGTAGAGTTCTGAAGGAGAACTACTGGTCTTATT
GTACACTTGCTGTACCTATTTTTTATTTAACAATATTCATCTATGGTATAATAAAGATGTCAT
GGTTGGAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 506

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96893
><subunit 1 of 1, 173 aa, 1 stop
><MW: 19733, pI: 8.78, NX(S/T): 0
MHWKMLLLLLLYNNAEASMCHRWSRAVLFPAAHRPKRSSSLPLNPVLQTSLEEVELLYEF
LLAELEISPDQLQISIKDEELASLRKASDFRTVCNNVIPKSIPDIRRLSASLSSHPGILKK
EDFERTVLTLAYTAYRTALSHGHQKDIWAQSLVSLFQALRHDLMRSSQPGVPP
```

Important features of the protein:

Signal peptide:

Amino acids 1-17

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 36-40;84-88;105-109

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FIGURE 507

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGC
CGGCCGAGCAATGCCAAGTGAGTACACCTATGTGAAACTGAGAAGTGATTGCTCGAGGCCTTC
CCTGCAATGGTACACCCGAGCTCAAAGCAAG**ATG**GAGAAGGCCAGCTTGTTATTTAAAGACAT
CCTCAAATGTACATTGCTTGTGTTTGGAGTGTGGATCCTTTATATCCTCAAGTTAAATTATAC
TACTGAAGAATGTGACATGAAAAAATGCATTATGTGGACCCTGACCATGTAAAGAGAGCTCA
GAAATATGCTCAGCAAGTCTTGCAGAAGGAATGTCGTCCCAAGTTTGCCAAGACATCAATGGC
GCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGA
CAGTGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCGGGAAGTTCTCCAGTAAAGTCCA
GACCCTCTTGGAACCTTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTG
GCGCTGTGTGGTTATTGGAAGCGGAGGAATACTGCACGGATTAGAACTGGGCCACACCCTGAA
CCAGTTCGATGTTGTGATAAGGTAAACAGTGCACCAGTTGAGGGATATTCAGAACATGTTGG
AAATAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGTCTGACCTTGAATATTAT
TCCAATGACTTATTTGTTGCTGTTTTATTAAAGAGTGTTGATTTCAACTGGCTTCAAGCAATG
GTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGGGAAGCAGGTGGCAGAAAAA
ATCCCACTGCAGCCAAAACATTTCAAGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTT
GACATCCTTCAGTACTCAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACA
ATCGGTGTCATTGCCGTTGTCTTAGCCACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTT
GGATATGACCTCAATCAACCCAGAACACCTTTGCACTACTTCGACAGTCAATGCATGGCTGCT
ATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCTTAAAGCTGGTCAAA
GAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTT**TGA**ACACAGAAAACCTCA
GTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGGACAGCCTTCTTGATGTATTTCTCCAT
CCTGCAGATACTTTGAAGTGCAGCTCATGTTTTTAACTTTTAAATTTAAAAACACAAAAAAAT
TTTAGCTCTTCCCCTTTTTTTTTTCTATTTATTTGAGGTCAGTGTTTGTGTTTGCACACCAT
TTTGTAATGAACTTAAGAATTGAATTGGAAAGACTTCTCAAAGAGAATTGTATGTAACGAT
GTTGTATTGATTTTTTAAGAAAGTAATTTAATTTGTAAACTTCTGCTCGTTTACACTGCACAT
TGAATACAGGTAACATAATTGGAAGGAGAGGGGAGGTCCTTTTGTGATGGTGGCCCTGAACCT
CATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTG
GAGAAGGTCACAACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGG
GAAGCTGTCTGGAGGTCCCTGGTGGAGAGGGACATAGAATCTGTGACCTCTGACAACCTGTG
AAGCCACCCTGGGCTACAGAAACCACAGTCTTCCCAGCAATTATTACAATTCTTGAATTCCTT
GGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCTAACGTGTTCCAGTGTCTGT
CTGAGGTGACTTAAAAAATCAGAACAAAACCTTCTATTATCCAGAGTCATGGGAGAGTACACCC
TTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCCAGTATTATAAATTGTGTA
TTTAA

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FIGURE 508

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYYTTEECMDMKMHYVDPDHVKRAQKYAQQVL
QKECRPKFAKTSMA LLFEHRYSDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLE
LLPEHDLPEHLKAKTCRRCVVIGSGGILHGLELGH TLNQFDVVIRLNSAPVEGYSEHVG N
KTTIRMTYPEGAPLS DLEYYSNDLFVAVLFKSVD FNWLQAMVKKETLPFWVRLEFFWKQVA
EKIPLQPKHFRILNPV IIKETA FDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEV
SLAGFGYDLNQPR TPLHYFDSQCMAAMNFQTMHNVTTETK FLLKLVKEGVVKDLSSGGIDR
EF
```

Important features of the protein:**Transmembrane domains:**

Amino acids 11-27;281-297

N-glycosylation sites:

Amino acids 30-34;180-184;334-338

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 2-6;109-113;223-227

N-myristoylation sites:

Amino acids 146-152;150-156;179-185;191-197

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FIGURE 509

GGGCGGACGCAGTGCAGTAAGAGCAGATGGGCGGACCCAAATTTCTTCGGCTTCACGATTTTG
CCGAGGTCTAGCCCTGCATCCAGCCTTGAAACAGGGTGGGGAGGAGGCAGAAAGGGGAGGGAC
TGCACTCCCTCTGAGCGTGCTAGCTCCGACTGCCTGACGGATCACCCCTCCGCTCCAACATGG
CTAGTTCCTCAACGCCGTGACTCAAGCCTGTTGTGCCAGGCAGGGCGCACTCAGCAGCGCAGC
CCCACAGGTGGCGAAGGCTCCGCGAGAGGGTTCCCGCCAGGCTAGACAGTGGAGTGCCGCACA
GCGCGCCTTCCAGCCTCGCAGCCGCCACCCTAGCGGTTCCGACCCGGCGCCAGCAGGCCTGCT
TGGTCGATCTTCGAGCCAAAG**ATG**CGGCGAGGCTGGAAGATGGCTCTGTCTGGGGGGCTGCGG
TGCTGCCGCCGGGTACTGTCTGGGTGCCAGTGCTCGTTATTGTCCTCGTCGTGCTCTGGTCC
TACTATGCCTACGTCTTTGAACTCTGCCTGGTTATTTACCTCATACTCTACCATGCCATCTTT
GTGTTCTTTACCTGGACCTACTGGAAGTCTATCTTTACACTCCACAGCAGCCAAACCAGAAG
TTCCACTTGTCCTACACAGACAAGGAGCGCTATGAAAATGAAGAAAGACCTGAGGTCCAGAAG
CAGATGCTTGTTGATATGGCCAAAAAGCTACCGGTTTACACAAGAACTGGAAGTGGAGGTCAG
TTCATCCAAAGGCAGCTAGAGAGGCAGCTCAGCAAGTATCTCAGAAAGGCTAAGTCATATATG
TTCTCAAAC**TAG**CCCTTTTTTTTCCTCCCATCTTCTGAAAACCACTATGGAGATTTTTCTCCA
CATTTTATTTCTAAAAAATTTTAAACACATATCAAAGCTGGAAGAATTGTATAGTAAACAAAC
TGTATACCCCAAACCTGGATTCTTCTGCTAACATTTTTCTGTGTTGCTATATCACATATCTATC
CACATATGCATACCTCTATTTATCTTTCGTCAAGCCATCTTATGTTTCTGATGCATTTCAAAG
TAAATAGCTGACATCAGTAAGACATCTACCTAAATATTTTATTCTGTTTTGTAAATTTACA
TACAAAAACATGCATAATCTTAAGGGTACCATTCCATGTATTTTGAAAAGTGTACACATCTGT
GTAACATAACCCCAATAAAATTGCCATCACCTCAG

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FIGURE 510

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98564
><subunit 1 of 1, 143 aa, 1 stop
><MW: 17255, pI: 9.99, NX(S/T): 0
MRRGWKMALSGGLRCCRRVLSWVPVLVIVLVVLWSYYAYVFELCLVIYLLILYHAIFVFFT
WTYWKSIFTLPQQPNQKFHLSYTDKERYENEERPEVQKQMLVDMAKKLPVYTRTGSGGQF
IQRQLERQLSKYLRKAKSYMFSN
```

Important features of the protein:**Transmembrane domain:**

Amino acids 24-45

N-myristoylation sites:

Amino acids 11-17;12-18

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FIGURE 511

CAGCCGGGGCGATGGCGGGGCTCTGGCTGGGGCTCGTGTGGCAGAAGCTGCTGCTGTGGGGCG
CGGCGAGTGCCCTTTCCCTGGCCGGCGCCAGTCTGGTCCTGAGCCTGCTGCAGAGGGTGGCGA
GCTACGCGCGGAAATGGCAGCAGATGCGGGCCATCCCCACGGTGGCCCGCGCCTACCCACTGGTG
GGCCACGCGCTGCTGATGAAGCCGGACGGGCGAGGTAAGGGCCGGCGCTCCTCCTGGAGCGCA
ACGGGGTCCGCAGCCCCGTTCCACCCCTCCGATCAGCCAGGAACCCGCTGCTTGTGGCGCTGG
CCGCAGGAGAGAGGAGCCTGTCACCCTGTGGAGAATGCACTCCCAGTTCTAGTCGTTGCCCT
TGGCACCCGCGGACACTGCTAGTGCCCCATCCCAAAGTGAGCATTCTTTGTGTGTAGCACA
GGATGCGGTATTTCCAAACCCCTGCCCTCGGTCTTTTCCACCTCACCGCTGCTCAGCTCTCA
AAGCCCTGCCGTTTCTCCTGCCTTGGCTTGGGAAGCCTTAGGAACAGAAGCTCCCTGGGAGC
ACAGAGCGGTTTTAAACTGGCCAACACCTTAACGCCCAGAGCCGCCCTCCTCTCGCTGCCACT
TTGGAAAATAAGAGACTAGAGATTCAGTGGACGCTTCCTCCCGGCATCACAAGACTTGACTGC
TGCTTCAGTTCCCGCTTGACCTTCATACTTTAGCCCTTTAAAGGATGTTACATAATAACAATT
AAGAGACGGCAGGGCCTTCAGGCAGACTTCTTTGGAGGGTGTCAAACGCCTTGTTTATTAAAG
AGTGAATTTTTTAATTAAAATCATGTTTTAAACAGAGATGGACATTTTATTGATGGAAAAAA
ATCACGTTAAGTTAGAAAGCTCTCAAAGTACCTGGTATTTACAACCTCCCTGTCAGGGAGGGC
GAACTCGATCTCAGAGTTTTATTTTCATCAGGGATTACGTTGAGGTACCCAGAAATGAGAAGA
TTTGCCCAAATGGCATATTTTTAAATTTGGCCAGACCAGAACCCAGTTTCCTCTGGGATTAT
TTGTTAGTAATCGTTTTTACAGGCTGAGCATTAACTAACTCCAAAGCTTGAAGGACTTTTTCTC
ATTTTCACTTGTTTTCTCTAATAAAAATAATGCTGTAATTTCAACTTCACAAGATGAGGCCTC
ATGGAAGAGTGTTTACCAAATATTTAAATACTTTGACAGAAAAAATCAAGCGAACTCTTT
GCCAACCAAATATCATCATGACTGATGTAACAAGTAATCCAACACAGATATGAAAATCACTGG
TAAAAATCATCTCAGTTAATTCTAAAAGCAGAGCTAACCACCCCTTTTGTCTAAGGCTTTAT
GGTATTTAAAAAATAAACTGTACAAAATATAGATTTTCCCCTATCCCCTACCCCTGGAAAGTA
ATATACTGAAGTCTCATCATACTGTTTTGGGGATTCCAGTAATTAAAATCTCTAGTGAACAAA
GACCTGTTTCAAACAACCTGTGAGCTGACTGGACTATTTAAAGTAATTCTCCTTGTAGTCAC
TTTCAGAGTGAAGACAATGACGAATACTGTCTTTTACAAAGGGACTTTTTTATTCCACCAACAA
ATTCTGGATTTTGGCATCAGGAAAACCACTGTTCAATTTCCAACACTATATCCAAGTTGTTTG
AGAAATTATTTAAACTCTTTAACTTAGAGGGTTTTCTTTCTCCTTTACTTGTTAAAGTGACT
ATATTACAGAGTCACTTTAAGGATTAAATTTATTGCATGCAAAGTTTCTAGATCACTGTCTAG
AAGTCAGTTAGAGTAAGTTCTTTAGTTGTCAATCAAGCATTTAGTAAGGCCCTGCTTTGTGCC
CAGTGTTGACCTCAACAAAGTTGGGGATATCAGAATATTCTAAGATACAGTCGTTGTTCCCAA
GAATCTTGCTTTTCACATACAAGAGGTGTTGCGTTTCATTTTGCGGCTAATGTCCAAACGCTG
GCCTCAGCCATTTACCTTGAAGATTGCAGTTGGCTTCCAACCTGGCCTCTAAACTCTAATCTA
GCATTTTCCAGTCCATTGTGACAAAGTCTGCCTTCCCCAGCTACTCCCAGCTGTTGGACCTGC
TGCCTTAGAACCACAGATTGGTACCTCGTGCC

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FIGURE 512

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA107443
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19353, pI: 10.97, NX(S/T): 0
MAGLWLGLVWQKLLLWGAASALSLAGASLVLSLLQRVASYARKWQOMRPIPTVARAYPLV
GHALLMKPDGRGKGRRSSWSATGSAAPFPPSDQPGTRCLWRWPQERGACHPVENALPVLV
VAPWHPPTLLVPHPKVSIFFVCSTGCGISKPLPSVFSLTLTAAQLSKPCRFLLPWLGKP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-25

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 75-79

N-myristoylation sites:

Amino acids 3-9;17-23;145-151

Amidation site:

Amino acids 73-77

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 513

GGCGGCTGGACGAGGACGCTCAGAGCCCAGCTCTCGAGAGTTCAAGCAACCGACGGTTCC
CCACTGCTCCCAGGAGCGGTTACCTGGGCACTCTGTGCCCCCTCCTTCCTGTTCTGGGCCCCA
GGCCGAGGACCTGCCAGTAGGGCTCAGTTGCCTGGAGCCCGTTTCAGCCCATCCCCCAGTT
CACTTTGCTTGTGGGATCTCCCCGTTGCTCCTGCCCCGTGGACTGAGTGGCAGGCCATCCT
ACAAGCACCCGGACACTTGACATCAGTGGTGTCAAGACAACCTCTAAGAAGGTTTTCCGTG
ATCCTGCAAGCCCTGCCTTCCTTCCTGGGATCCTGCCTTCAATTTGATTGCACAGGTACC
ACAGCAAGCCAGTGCTGTGTGCTCCGAGTTCCAGGGCGTCCCTCCAGCTCAGCCACTGCAC
TGAGAACATGGACTCTCTGTGGGGCCCAGGAGCCGGGAGTCACCCCCTTTGGGGTCCACAA
CACCCGGCTGTCCCCAGACTTGTGTCCAGGGAAGATAGTGTGAGGGCCCTCAAGGAGAG
CGGGGCAGGGATGCCTGAGCAGGACAAGGACCCTAGAGTCCAAGAGAATCCTGGTGATCA
GAGAAGGGTCCCCGAGGTCACCGGGGATGCACGGTCTGCATTTCTGGCCCCCTGCGGGACAA
TGGAGGCCTCTCTCCCTTTGTGCCCCGGGCCCTCTGCAGACAGACCTCCATGCCCA
GAGGTCAGAAATCAGATATAACCAGACATCCCAGACCTCCTGGACGAGCTCCTGCACCAA
CCGAAATGCCATCTCCAGCTCCTACAGCTCCACGGGAGGCTTGCTGGGGCTAAAGCGGAG
GAGGGGGCCAGCCTCATCCCCTGCCAGCTGACCCTCAGTTCCTCAAAGACAGTGAGTGA
GGACAGGCCTCAGGCTGTCTCTTCAGGTCACACCCAGTGTGAAAAGGCAGCAGATATAGC
ACCAGGGCAGACACTCACCTCAGGAATGACTCCTCCACATCCGAGGCCTCTAGGCCCCAG
TACACACAAGTTTCCCCTGCTGCCACGCAGGCGAGGGGAGCCTTTGATGCTGCCACCTCC
CTTAGAGCTGGGGTACCGGGTCACTGTTGAAGACCTGGACCGGGAGAAGGAGGCGGCCTT
CCAGCGCATCAACAGTGCAGTGCAGGTTGAGGACAAGGCCATCTCGGACTGCAGACCCTC
ACGGCCTTCCCACACTTTGTCCTCACTTGCAACAGGGGCTTCTGGTCTGCCTGCCGTTTC
TAAAGCACCCAGTATGGATGCACAGCAGGAGACACACAAGTCCCAAGACTGCCTGGGCCT
ACTGGACCCCTTAGCATCTGCTGCAGGGGTCCCCTCTACAGCTCCCATGTCTGGGAAGAA
GCACAGACCACCAGGCCCCCTGTTCTCCTCCTCAGATCCCCCTTCCTGCCACCTCTTCTGA
TTCCCAGGACTCAGCCCAGGTCACCTCGCTGATTCCTGCCCCCTTCCCAGCTGCAAGCAT
GGATGCGGGCATGAGAAGAACAAGGCATGGCACTTCTGCTCCTGCAGCTGCCGCAGCAGC
CCCTCCCCGCTCCACATTGAACCCACGTTGGGGTCACTACTGGAGTGGATGGAGGCCCT
TCACATTTCTGGGCCTCAGCCACAGCTGCAGCAGGTGCCCAGAGGTCAGAACCAGAGATC
CCAGACCTCCTGGACCAGCTCGTGCCCCAAATGAAATGCCATCTCGAGCCCCCTACAGCTC
TACGGGAGGCCTCCCGGAACAAAAGCGGAAGAGGGGCCAGCCTCATCCCCTGCCCAGCTG
ACCCTCAGTTCCTCAAACACAGTGAGTGAGGACGGACCTCAGGCTGTCTCTTCGGGTAC
ACCCAGTGTGAAAAGACGGCAGATACAGCACCAGGGCAGACACTCGCCTCCAGGGGTGGC
TCCCCCAGATCCCAGGCCTCTAGGCCCCGTATATGCAAGTTTCCCCTGCTGCCACGCAGG
CGAGGGGAGCCTTTGATGCTGCCACCTCCCTTAGAGATGGGGTACCGGGTCACTGCTGAA
GACCTGGACCGGGAGAAGGAGGAGGCATTCCAGCGCATCAACAGTGCAGTGCAGGTTGAG
GACCAGGCCATCTAGGACTGCAGACCCTCACGGCCTTCCCACACTTTGTCCTCACTTGCA
ACAGGGGCTTCTGGTCTGCCTGCCGTTTCTAAAGCACCCAGTATGGATGCACAGCAGGAG
ACACACAAGTCCCAAGACTGCCTGGGCCTAGTGGCCCCCTGCATCTGCTGCACAGGCCT
GTAGTCCCAGCTACTTGGGAGGCTGAGGCAGGAGAACGGCATAAACCCGGGAGGCAGAGC
TTGCAGTGAGCTGAGATCGCGCCACTGCACTCCAGCCTGGGTGACAGAGCGAGACTCCGT
CTC

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FIGURE 514

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA107786
><subunit 1 of 1, 428 aa, 1 stop
><MW: 45450, pI: 9.28, NX(S/T): 3
MDSLWGPAGSHPFVHNTRLSPDLCPGKIVLRALKESGAGMPEQDKDPRVQENPGDQRR
VPEVTGDARSAFRPLRDNGGLSPFVPGPGPLQTDLHAQRSEIRYNQTSQTSWTSSCTNRN
AISSSYSSSTGGLLGLKRRRGPASSHCQLTLSSSKTVSEDRPQAVSSGHTQCEKAADIAPG
QTLTLRNDSSSTSEASRPSTHKFPLLPRRRGEPLMLPPPLELGYRVTVEDLDREKEAAFQR
INSALQVEDKAISDCRPSRPSHTLSSLATGASGLPAVSKAPSMDAQQETHKSQDCLGLLD
PLASAAGVPSTAPMSGKKHRPPGPLFSSSDPLPATSSDSQDSAQVTSIPAPFPAASMDA
GMRRTRHGTSAPAAAAAAPPSTLNPTLGSLLEWMEALHISGPQPQLQQVPRGQNQRSQT
SWTSSCPK

Important features of the protein:**N-glycosylation sites:**

Amino acids 105-109;187-191

Glycosaminoglycan attachment site:

Amino acids 38-42

N-myristoylation sites:

Amino acids 15-21;130-136;180-186;307-313;361-367

Amidation site:

Amino acids 315-319

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 106-117

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FIGURE 515

GTCAGGGCCAGGGTGAGCGCCCGACTCCGAGCTGTCCCCGCTCCCGGCGCGGGCGCTCCGCTCT
CAGCCACCTCACGGCTGCCAGGAGTGCGCGGGAGTTTGCCCCGGAGCGCGGGGAAGTTTCCTC
CGAAGCTGCGCTCCTGGAACAGCAGCACCTGCAAGCGCCCGGCAGCGGCCCCGCGAGGTTACTT
TATGGAATTGGGCTCTTAGAGAACAAAGAAAGACTGAAGTTTTACGGGAAAACAAATCATGTG
GTCTTCAGATTCTGAAATAAGGAGAAATGCAGCCATCTGAAATGGTCATGAACCCCCAAACAAG
TCTTCCTCTCTGTGCTGATATTTGGAGTAGCTGGGCTACTCCTCTTCATGTATTTGCAAGTCTGG
ATTGAAGAACAACATACAGGGAGAGTGGAGAAGAGAAGAGAACAAAAAGTAACTTCAGGATGG
GGACCAGTGAAGTACTTGCGGCCTGTACCCAGAATCATGAGTACAGAAAAAATCCAGGAACAT
ATCACCAACCAGAACCCCAAGTTTCACATGCCTGAGGATGTACGAGAAAAAAGGAAAATCTT
CTACTCAATTCTGAGAGATCTACTAGGCTCTTAACAAAGACCAGTCATTCAACAAGGAGGGGAT
CAAGCTTTAAGTAAGTCCACAGGGTCAACCAACAGAGAAGTTGATTGAAAAACGTCAAGGAGCT
AAGACTGTTTTTAACAAGTTCAGCAACATGAATTGGCCAGTGGACATTCAACCTTTAAACAAA
AGTTTAGTCAAAGATAATAAATGGAAGAAAAGTGAAGGAGACCCAAGAGAAACGAAGGTCTTTC
CTTCAGGAGTTTTGCAAGAAATACGGTGGGGTGAGTCATCATCAGTCACATCTTTTTTCATACA
GTATCCAGAATCTATGTAGAAGATAAACACAAAATCTTATATTGTGAGGTACCTAAGGCTGGC
TGTTCCAATTGGAAAAGAATTCTGATGGTACTAAATGGATTGGCTTCCTCTGCATACAACATC
TCCCACAATGCTGTCCACTACGGGAAGCATTGGAAGAAGCTAGATAGCTTTGACCTAAAAGGG
ATATATAACCGCTTAAATACTTACACCAAAGCTGTGTTTGTTGCTGATCCCATGGAAAGATTA
GTATCAGCCTTTAGGGACAAATTTGAACACCCCAATAGTTATTACCATCCAGTATTCGGAAAG
GCAATTATCAAGAAATATCGACCAAATGCCTGTGAAGAAGCATTAAATTAATGGATCTGGAGTC
AAGTTCAAAGAGTTTATCCACTACTTGCTGGATTCCCACCGTCCAGTAGGAATGGACATTCAC
TGGGAAAAGGTCAGCAAACCTCTGCTATCCGTGTTTGATCAACTATGATTTTGTAGGGAAATTT
GAGACTTTGGAAGAAGATGCCAATTACTTTTTTACAGATGATCGGTGCTCCAAAGGAGCTGAAA
TTTCCCAACTTTAAGGATAGGCACTCTTCCGATGAAAGAACCAATGCTCAAGTCGTGAGACAG
TATTTAAAGGATCTGACTAGAACTGAGAGACAATTAATCTATGACTTTTATTACTTGGACTAT
TTAATGTTTAAATTATACAACCTCCACTTTTGTAGTTTGCATTCATTTTCTAAAACCTGTATAT
ACTTAATGATGATAAGTTCAAATCAGCTGTAATTTTTCTATAATTCTCTGTATGACAGAAATT
TAACCAAGTGCAGTTGTCTTGATTTAATGTAGATTTTTTACCAAATAGTATGACACCAATTGGC
ACAAAGTTATAGGAAAATCACCTACAGGAGATGTAAACAACCTTGAGTTGCTCTAAAATGTTTG
GAAAAGAGCTGCTTTTGCATTATGAATTATATTGTTGAAGCAATAACCTAGCCAGCTGTTGCA
TTAGCTAAAGCAGCCTCTTGCAATGGTAGGAAAAAAGGATCTCAAATAGCATGAGTGTATGTC
TATATCCTGAAATTTATTGTCTAAAATGCATGAATATATTTTTTAGCAGTCTGTGGCATATTAA
TCAAACCTGTTGAATTGTTTTCTTACACCTGGAAATCTTTCTATCAACTATAATGATAAATCC
ATTTTGAAGTGATATTTTGGACTTAGGCATTTTACTTTAGATTGGAAGGCATTATGTGATTTACA
ATATGAGAATATAGCAGAAAAACCA

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FIGURE 516

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108682
><subunit 1 of 1, 443 aa, 1 stop
><MW: 52021, pI: 9.63, NX(S/T): 4
MQPSEMVMNPKQVFLSVLIFGVAGLLLFMYLQVWIEEQHTGRVEKRREQKVTSGWGPVKY
LRPVPRIMSTEKIQEHITNQNPKFHMPEDVREKKENLLLNSERSTRLLTKTSHSQGGDQA
LSKSTGSPTEKLEKROGAKTVFNKFSNMNWPVDIHPLNKSLVKDNKWKKTEETQEKRRS
FLQEFCKKYGGVSHHQSHLEHTVSRIYVEDKHKILYCEVPKAGCSNWKRIILMVLNGLASS
AYNISHNAVHYGKHLKKLDSFDLKGIIYTRLNTYTKAVFVRDPMERLVSFRDKFEHPNSY
YHPVFGKAIKKYRPNACEEALINGSGVKFEFEFIHYLLDSHRPVGMDIHWEKVSKLCYPC
LINYDFVGKFETLEEDANYFLOMIGAPKELKFPNFKDRHSSDERTNAQVVRQYLKDLTRT
ERQLIYDFYYLDYLMFNYYTPLL

Important features of the protein:**Signal peptide:**

Amino acids 1-24

N-glycosylation sites:

Amino acids 159-163;243-247;324-328;437-441

Glycosaminoglycan attachment site:

Amino acids 53-57

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 177-181

Tyrosine kinase phosphorylation site:

Amino acids 329-337

N-myristoylation sites:

Amino acids 116-122;236-242

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FIGURE 517

GGAACCTCCAGGCACCCCTGTGTGGCCGCACTGCTCCCTCTGGCCCAACCATGCTCTGTCCAGCCACCTGCTGC
CCGCCTTGGTCCTGTTCTTGGCAGGGTCCTCAGGCTGGGCCTGGGTCCCCAACCACTGCAGGAGCCCTGGCCAGG
CCGTGTGCAACTTCGTGTGTGACTGCAGGGACTGCTCAGATGAGGCCAGTGTGGTTACCACGGGGCCTCGCCCA
CCCTGGGCGCCCCCTTCGCCTGTGACTTCGAGCAGGACCCCTGCGGCTGGCGGGACATTAGTACCTCAGGCTACA
GCTGGCTCCGAGACAGGGCAGGGGCGCACTGGAGGGTCCTGGGCCTCACTCAGACCACACACTGGGCACCGACT
TGGGCTGGTACATGGCCGTTGGAACCCACCGAGGGAAAGAGGCATCCACCGCAGCCCTGCGCTCGCCAACCCTGC
GAGAGGCAGCCTCCTCTTGCAAGCTGAGGCTCTGGTACCACGCGGCCTCTGGAGATGTGGCTGAACTGCGGGTGG
AGCTGACCCATGGCGCAGAGACCCTGACCCTGTGGCAGAGCACAGGGCCCTGGGGCCCTGGCTGGCAGGAGTTGG
CAGTGACCACAGGGCCGCATCCGGGGTGACTTCCGAGTGACCTTCTCTGCCACCCGAAATGCCACCCACAGGGGCG
CTGTGGCTCTAGATGACCTAGAGTTCTGGGACTGTGGTCTGCCACCCCGGAGCCAACTGTCCCCGGGACACC
ACCACTGCCAGAACAAAGGTCTGCGTGGAGCCCCAGCAGCTGTGCGACGGGGAAGACAACCTGCGGGGACCTGTCTG
ATGAGAACCCACTCACCTGTGGCCGCCACATAGCCACCGACTTTGAGACAGGCCTGGGCCCATGGAACCGCTCGG
AAGGCTGGTCCCGGAACCACCGTGTGGTGGTCCCTGAGCGCCCTCCTGGCCACGCGTGACCACAGCCGGAACA
GTGCACAGGGCTCCTTCTGCTCTCGTGGCCGAGCCTGGCACCCCTGCTATACTCTCCAGCCCCGAATTCCAAG
CCTCAGGCACCTCCAACCTGCTCGCTGGTCTTCTATCAGTACCTGAGTGGGTCTGAGGCTGGCTGCCTCCAGCTGT
TCCTGCAGACTCTGGGGCCCGGCGCCCCCGGGCCCCCGTCTGCTGCGGAGGCGCCGAGGGGAGCTGGGGACCG
CCTGGGTCCGAGACCGTGTGACATCCAGAGCGCCTACCCCTTCCAGATCCTCCTGGCCGGGACAGAGGCCCGG
GGGGCGTCTGGGTCTGGACGACCTCATCCTGTCTGACCACTGCAGACCAGTCTCGGAGGTGTCCACCCTGCAGC
CGCTGCCTCCTGGGCCCGGGCCCCAGCCCCCAGCCCTGCGGCCAGCTCGCGGCTCCAGGATTCCTGCAAGC
AGGGGCATCTTGCTGCGGGGACCTGTGTGTGCCCCCGGAACAACCTGTGTGACTTCGAGGAGCAGTGCGCAGGGG
GCGAGGACGAGCAGGCCTGTGGCACACAGACTTTGAGTCCCCCGAGGCTGGGGGCTGGGAGGACGCCAGCGTGG
GGCGGCTGCAGTGGCGGCTGTCTCAGCCCAGGAGAGCCAGGGGTCCAGTGCAGCTGCTGCTGGGCACTTCCTGT
CTCTGCAGCGGGCCTGGGGGACGCTAGGCGCTGAGGCCCGGCTCCTCACACCCCTCCTTGGCCCTTCTGGCCCA
GCTGTGAACTCCACCTGGCTTATTATTTACAGAGCCAGCCCCGAGAGGTCTCCTGTAACTTTGAGCGGGACACAT
GCAGCTGGTACCCAGGCCACCTCTCAGACACACACTGGCGCTGGGTGGAGAGCCGCGGCCCTGACCACGACCACA
CCACAGGCCAAGGCCACTTTGTGCTCCTGGACCCACAGACCCCTGGCCTGGGGCCACAGTGCCACCTGCTCT
CCAGGCCCCAGGTGCCAGCAGCACCACGGAGTGTCTCAGCTTCTGGTACCACCTCCATGGGCCCCAGATTGGGA
CTCTGCGCCTAGCCATGAGACGGGAAGGGGAGGAGACACACCTGTGGTCTGCGGTGAGGCACCCAGGGCAACCGCT
GGCACGAGGCCTGGGCCACCCCTTCCCACAGCCTGGCTCCCATGCCAGTACCAGCTGCTGTTGAGGGCCTCC
GGGACGGATACCACGGCACCATGGCGCTGGACGATGTGGCGTGGCGCCGGGCCCTGCTGGGCCCTAATTACT
GCTCCTTTGAGGACTCAGACTGCGGCTTCTCCCTGGAGGCCAAGGTCTCTGGAGCGGCAGGCCAATGCCTCGG
GCCATGCTGCCTGGGGCCCCCAACAGACCATAACCTGAGACAGCCCAAGGGCACTACATGGTGGTGGACACAA
GCCCAGACGCACTACCCCGGGGCCAGACGGCCTCCCTGACCTCCAAGGAGCACAGGCCCTGGCCAGCCTGCTT
GTCTGACCTTCTGGTACCACGGGAGCCTCCGCGAGCCAGGCACCCCTGCGGGTCTACCTGGAGGAGCGCGGGAGGC
ACCAGGTGCTCAGCCTCAGTGCCACGGCGGGCTTGCCTGGCGCCTGGGCAGCATGGACGTGCAGGCCGAGCGAG
CCTGGAGGGTGGTGTGTTGAGGCAGTGGCGCAGGCGTGGCACACTCCTACGTGGCTCTGGATGATCTGCTCCTCC
AGGACGGGCCCTGCCCTCAGCCAGGTTCCTGTGATTTTGAAGTCTGGCCTGTGTGGCTGGAGCCACCTGGCCGGGC
CCGGCCTGGGCGGATACAGCTGGGACTGGGGCGGGGGAGCCACCCCTCTCGTTACCCCGAGCCCCCTGTGGACC
ACACCCTGGGCACAGAGGCAGGCCACTTTGCCTTCTTTGAAACTGGCGTGTGGGCCCGGGGGCCGGGCCGCT
GGCTGCGCAGCGAGCCTCTGCCGGCCACCCAGCCTCCTGCCTCCGCTTCTGGTACCACATGGGTTTTCTGAGC
ACTTCTACAAGGGGGAGCTGAAGGTACTGCTGCACAGTGTCTCAGGGCCAGCTGGCTGTGTGGGGCGCAGGCGGGC
ATCGGCGGCACCACTGGCTGGAGGCCAGGTGGAGGTAGCCAGTGCCAAGGAGTTCCAGATCGTGTGTTGAAGCCA
CTCTGGGCGGCCAGCCAGCCCTGGGGCCCATTGCCCTGGATGACGTGGAGTATCTGGCTGGGCAGCATTGCCAGC
AGCCTGCCCCAGCCCCGGGGAACACAGCCGCACCCGGGTCTGTGCCAGCTGTGGTTGGCAGTGCCCTCCTATTGC
TCATGCTCCTGGTGTGCTGGGACTTGGGGGACGGCGCTGGCTGCAGAAGAAGGGGAGCTGCCCCCTTCCAGAGCA
ACACAGAGGCCACAGCCCCTGGCTTTGACAACATCCTTTTCAATGCGGATGGTGTCAACCCTCCCGGCATCTGTCA
CCAGTGATCCGTAGACCACCCAGACAAGGCCCGCTTCTCAGTGACATCCAGCACTTGGTCAGACCCTAGCC
AGGGACCGGACACCTGCCCCGCCAGGCTGGGACAGGCTGCAGGTCTCAGGATATGCTGAGGCCTGGGCGTTCCC
TGCCCTGTGCTGACTCTGTTGCTCTGTGAATAAACACCCTGGCCCATGAGGGCCGCCCAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

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FIGURE 518

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108684
><subunit 1 of 1, 1137 aa, 1 stop
><MW: 122776, pI: 6.00, NX(S/T): 4
MPLSSHLLPALVLFFLAGSSGWAVPNHCRSPGQAVCNFVCDRCDCSDEAQCQGYHGASPTL
GAPFACDFEQDPCGWRDISTSGYSWLRDRAGAALEGPGPHSDHTLGTDLGWYMAVGTHRG
KEASTAALRSPTLREAASSCKLRLWYHAASGDVAELRVELTHGAETTLWQSTGPGWPGW
QELAVTTGRIRGDFRVTF SATRNATHRGAVALLDLEFWDCGLPTPQANCPPGHHHCQNKV
CVEPQQLCDGEDNCGDLSDENPLTCGRHIATDFETGLGPWNRSEGWSRNRHAGGPERPSW
PRRDHSRNSAQGSFLVSVAEPGTPAILSSPEFQASGTSNCSLVFYQYLSGSEAGCLQLFL
QTLGPGAPRAPVLLRRRRGELGTAWVRDRVDIQSAYPFQILLAGQTGPGGVVGLDDLILS
DHCPRVSEVSTLQPLPPGPRAPAPQPLPPSSRLQDSCKQGHLAGDLCVPPEQLCDFEEQ
CAGGEDEQACGTTDFESPEAGGWEDASVGRQLQWRRVSAQESQGSSAAAAGHFLSLQRAWG
QLGAEARVLTPLLGPSPGSCLEHLAYYLSQPREVSCNFERDTCWYPGHLSDTHWRWVE
SRGPDHDHTTGQGHFVLLDPTDPLAWGSAHLLSRPQVPAAPTECLSFYHHLHGPGQIGTL
RLAMRREGEETHLWSRSGTQGNRWHEAWATLSHQPGSHAQYQLLFEGLRDGYHGTMALDD
VAVRPGPCWAPNYCSFEDSDCGFSPPGGQGLWRRQANASGHAAGPPTDHTTETAQGHYMV
VDTSPDALPRGQTASLTSKEHRPLAQPACLTFWYHGSLRSPGTLRVYLEERGRHQVLSLS
AHGGLAWRLGSMQVQAEARWRVFEAVAAGVAHSYVALDDLLQLDGPQPGSCDFESGL
CGWSHLAGPGLGGYSWDWGGGATPSRYPQPPVDHTLGTEAGHFAFFETGVLGPGGRAAWL
RSEPLPATPASCLRFWYHMGFPEHFYKGEKLVLLHSAQGQLAVWGAGGHRHQLWLEAQVE
VASAKEFQIVFEATLGGQPALGPALDDVEYLAGQHCQPPAPSPGNTAAPGSVPAVVGSA
LLLLMLLVLLGLGGRRWLQKKGSCPFQSNTEATAPGFDNILEFNADGVTLPASVTS DP
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 1075-1092

N-glycosylation sites:

Amino acids 203-207;281-285;339-343;756-760

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 514-518;1100-1104

N-myristoylation sites:

Amino acids 32-38;55-61;61-67;106-112;116-122;336-342;350-356;409-415;
523-529;540-546;678-684;707-713;791-797;870-876;921-927;
937-943;954-960;1036-1042;1071-1077

Amidation site:

Amino acids 1093-1097

Cell attachment sequence:

Amino acids 191-194

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FIGURE 519

GCAGGGGAGCTCCGAGTGTCCACAGGAAGGGAACCTATCAGCTCCTGGCATCTGTAAGGATGCT
GTCCATGCTGAGGACAATGACCAGACTCTGCTTCCTGTTATTCTTCTCTGTGGCCACCAGTGG
GTGCAGTGCAGCAGCAGCCTCTTCTCTTGAGATGCTCTCGAGGGAATTCGAAACCTGTGCCTT
CTCCTTTTCTTCCCTGCCTAGAAAGCTGCAAAGAAATCAAGGAACGCTGCCATAGTGCAGGTGA
TGGCCTGTATTTTCTCCGCACCAAGAATGGTGTGTCTACCAGACCTTCTGTGACATGACTTC
TGGGGGTGGCGGCTGGACCCTGGTGGCCAGCGTGACGAGAATGACATGCGTGGGAAGTGCAC
GGTGGGTGATCGCTGGTCCAGTCAGCAGGGCAACAAAGCAGACTACCCAGAGGGGGATGGCAA
CTGGGCCAACTACAACACCTTTGGATCTGCAGAGGCGGCCACGAGCGATGACTACAAGAACCC
TGGCTACTACGACATCCAGGCCAAGGACCTGGGCATCTGGCATGTGCCCAACAAGTCCCCCAT
GCAGCATTGGAGAAACAGCGCCCTGCTGAGGTACCGCACCAACACTGGCTTCCTCCAGAGACT
GGGACATAATCTGTTTGGCATCTACCAGAAATACCCAGTGAAATACAGATCAGGGAAATGTTG
GAATGACAATGGCCCAGCCATACCTGTGGTCTATGACTTTGGTGATGCTAAGAAGACTGCATC
TTATTACTCACCGTATGGTCAACGGGAATTTGTTGCAGGATTCGTTTCAGTTCCGGGTGTTTAA
TAACGAGAGAGCAGCCAACGCCCTTTGTGCTGGGATAAAAGTTACTGGCTGTAACACTGAGCA
TCACTGCATCGGTGGAGGAGGGTTCTTCCCACAGGGCAAACCCCGTCAGTGTGGGGACTTCTC
CGCCTTTGACTGGGATGGATATGGAACCTCACGTTAAGAGCAGCTGCAGTCGGGAGATAACGGA
GGCGGCTGTACTCTTGTTCTATAGATGAGACAGAGCTCTGCGGTGTCAGGGCGAGAACCCATC
TTCCAACCCCGGCTATTTGGAGACGGAAAACTGGAATTCTAACAAGGAGGAGAGGAGACTAA
ATCACATCAATTTGCA

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FIGURE 520

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108701
><subunit 1 of 1, 325 aa, 1 stop
><MW: 36212, pI: 8.68, NX(S/T): 1
MLTMLRTMTRLCLLFFSVATSGCSAAAASSLEMLSREFETCAFSFSSLPRSCKEIKERC
HSAGDGLYFLRTKNGVVYQTFCDMTSGGGGWTLVASVHENDMRGKCTVGDRWSSQQGNKA
DYPEGDGNWANYNTFGSAEAATSDDYKNPGYYDIQAKDLGIWHVPNKSPMQHWRNSALLR
YRTNTGFLQRLGHNLFGIYQKYPVKYRSGKCWNDNGPAIPVVYDFGDAKKTASYYSYPYGO
REFVAGFVQFRVFNNERAANALCAGIKVTGCNTEHHCIGGGGFFPQGKPRQCGDFSADFWD
DGYGTHVKSSCSREITEAAVLLFYR

Important features of the protein:**Signal peptide:**

Amino acids 1-26

Glycosaminoglycan attachment site:

Amino acids 86-90

N-myristoylation sites:

Amino acids 23-29;88-94;127-133;136-142;265-271

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FIGURE 521

GATCAGTGTGTGAGGGAAGTCCCATCATGAGGTCTGACAAGTCAGCTTTGGTATTTCTGCTCCTGCAGCTCTTCT
GTGTTGGCTGTGGATTCTGTGGGAAAGTCCTGGTGTGGCCCTGTGACATGAGCCATTGGCTTAATGTCAAGGTCA
TTCTAGAAGAGCTCATAGTGAGAGGCCATGAGGTAACAGTATTGACTCACTCAAAGCCTTCGTTAATTGACTACA
GGAAGCCTTCTGCATTGAAATTTGAGGTGGTCCATATGCCACAGGACAGAACAGAAGAAAATGAAATATTTGTTG
ACCTAGCTCTGAATGTCPTGCCAGGCTTATCAACCTGGCAATCAGTTATAAAATTAAATGATTTTTTTTGTGAA
TAAGAGGAACCTTTAAAAATGATGTGTGAGAGCTTTATCTACAATCAGACGCTTATGAAGAAGCTACAGGAAACCA
ACTACGATGTAATGCTTATAGACCCTGTGATTCCCTGTGGAGACCTGATGGCTGAGTTGCTTGCAGTCCCTTTTG
TGCTCACACTTAGAATTTCTGTAGGAGGCAATATGGAGCGAAGCTGTGGGAACTTCCAGCTCCACTTTCCTATG
TACCTGTGCCTATGACAGGACTAACAGACAGAATGACCTTTCTGGAAAGAGTAAAAAATTCATGCTTTCAGTTT
TGTTCCACTTCTGGATTACGAGTATCATTTTTTGGGAAGAGTTTTATAGTAAGGCATTAGGAAGGCCCA
CTACATTATGTGAGACTGTGGGAAAAGCTGAGATATGGCTAATACGAACATATTGGGATTTTGAATTTCTCAAC
CATACCAACCTAACTTTGAGTTTGTGGAGGATTGCACTGTAAACCTGCCAAAGCTTTGCCTAAGGAAATGGAA
ATTTTGTCCAGAGTTCAGGGGAAGATGGTATTGTGGTGTCTCTGGGGTCACTGTTTCAAATGTTACAGAAG
AAAAGGCTAATATCATTGCTTCAGCCCTTGCCAGATCCACAGAAGGTGTTATGGAGGTACAAAGGAAAAAAC
CATCCACATTAGGAGCCAATACTCGGCTGTATGATTGGATACCCAGAATGATCTTCTTGGTCATCCCAAACCA
AAGCTTTTATCACTCATGGTGGAATGAATGGGATCTATGAAGCTATTTACCATGGGGTCCCTATGGTGGGAGTTC
CCATATTTGGTGATCAGCTTGATAACATAGCTCACATGAAGGCCAAAGGAGCAGCTGTAGAAATAAACTTCAAAA
CTATGACAAGCGAAGATTTACTGAGGGCTTTGAGAACAGTCATTACCGATTCTCTTATAAAGAGAATGCTATGA
GATTATCAAGAATTCACCATGATCAACCTGTAAAGCCCCTAGATCGAGCAGTCTTCTGGATCGAGTTTGTCTATGC
GCCACAAAGGAGCCAAGCACCTGCGATCAGCTGCCCATGACCTCACCTGGTTCCAGCACTACTCTATAGATGTGA
TTGGGTTCTGTGCTGACCTGTGTGGCAACTGCTATATTCTTGTTCACAAAATGTTTTTTATTTTCTGTCAAAAAT
TTAATAAACTAGAAAGATAGAAAAGAGGGAATAGATCTTTCCAAATTCAAGAAAGACCTGATGGGGTAATCCTG
TTAATTCAGCCACATAGAATTTGGTGAAAACCTTGCTATTTTTCATATTATCTATTCTGTTATTTTATCTTAGCT
ATATAGCCTAGAATTCATGATCATGAGGTTGTGAGTATATCTCATTCTTTCTGTTGATTTTCTTAGGTGTCTTT
ACTCTCTTCTCTCACTTTGTGACACAAGGACATGAATACATCTAAATTTTCTATTTCTGATATGACTGTTTTGA
TGATGTCATTACTTCTATAACCTTAAGTGATAGGGTGACATGCAATATGATTATTCCTGGTGTGCGCCCAAACAC
ATGGATATAAAGAGGTAAAAAATTAATAATTCACAAAATTCAGTAAACCACACAAATCAGGTAAGTGTCTATGA
GATTAGCTGGCTATGAGAAACATAATGATGTTTCTTTTTCAATTTAAATAAGCCTTTCTACATAGCCAGCATCAG
TGATCTCAGAAAATAAATTGCTAATAATGATGACATGGCATTATGCTTAGAAAAGTTTGCTGTATTTCCATAGAC
CTCATCTAGATGTCATGGCCTACATTTCTGCCATCACTCAACCAATACTTTTTTCTGTTTTCTTGATGATAAAAA
GACCTTTCTCATGATTGCCATCAAATAACAAAAGAACTATTTTTTTTCTCACATAGAGAACATGTCAGTAAGAT
ATTCAAGGTGAACAGATATTTTTGGGATTAGTAACCTATTTGAAATATGTGGTGATAATTACTGAGTTTATAAAAT
TTATTTGATAGTACACTTAAAGAAGATTTATATGTTTATTCTTTAAAAATGATGAATACTCATAATTCTTATCTC
TATAATCAAAGTATAATTTACTGTAGAAAAATAAAGAGATGCTTGTCTGAAAGTAAGATCAGTGAAGTGTCTT
TCAGTCTCAATCTTTGAGAATTGTAAATTCATCAAATAATTGCTTACATAGTAAAAATTTAAGGTATTAGAAAAC
CTGCATAACAAATAGTATTATATATTAATAATTTTGATATGTAAAGCTCTACACAAAGCTAAATATAGTGTAATA
ATGTTTACACTAGTAAGCAAATATGTTAATCTTCTCATTTTTTTACTGTATATAATCTTAGTGATATGCCTATT
AATAGTTTTAAATAAATAAATTGGCTTATCTGGCTTTTTGAAAATTTTGAATTTCTTACAGATGTTGATTAGGTA
TATCTACAAATTAATTTCAATTTTAAATGATGATATAAAAAATAAATAAGTATTTTTCTTGTGTATGTATACA
ATAAATATAAATAAATTTGTTTACTGTTTTGAAAGTTTCTTAAGTTTAA

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FIGURE 522

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108720
><subunit 1 of 1, 527 aa, 1 stop
><MW: 60284, pI: 8.31, NX(S/T): 3
MRSDKSALVFLLLQLFCVGCFCGKVLVWPCDMSHWLNVKVILEELIVRGHEVTVLTHSK
PSLIDYRKPSALKFEVVHMPQDRTEENEIFVDLALNVLPGLSTWQSVIKLNDFVEIRGT
LKMMCESFIYNQTLMKKLQETNYDVMLIDPVI PCGDLMAELLAVPFVLT LRISVGGNMER
SCGKLPAPLSYVPVPM TGLTDRMTFLERVKNSMLS VLFHFWIQDYDYHFWEEFYSKALGR
PTTLCETVGKAEIWLIRTYWDFEFPQPYQPNFEFVGGLHCKPAKALPKEMENFVQSSGED
GIVVFSLSLGFQNVTEEKANIIASALAQIPQKVLWRYKGKKPSTLGANTRYLDWIPQNDL
LGHPKTKAFITHGGMNGIYEAIYHGVPMVGVPIFGDQLDNIAHMKAKGA AVEINFKTMTS
EDLLRALRTVITDSSYKENAMRLSRIHHDQPVKPLDRAVFWIEFVMRHKGAKHLRSA AHD
LTFQHYSIDVIGFLLTCVATAIFLFTKCF LFSCQKFNKTRKIEKRE

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 489-510

N-glycosylation sites:

Amino acids 131-135;313-317;518-522

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 67-71;340-344

Tyrosine kinase phosphorylation sites:

Amino acids 122-131;136-144

N-myristoylation sites:

Amino acids 19-25;276-282;373-379;377-383

Amidation site:

Amino acids 338-342

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FIGURE 523

GGCTGCGGGGTCTGGCACGGAAGATGCACGCGAGGCTCCTGGGGCTCTCGGCCCTGCTGCAGGC
GGCCGAACAGAGCGCGCGCCTTTACACCGTGGCTTACTACTTCACCACAGGACGGCTTCTGTG
GGGGTGGCTGGCCCTTGCTGTCCTCCTGCCCGGGTTCTTGGTCCAGGCCCTGAGCTACCTGTG
GTTCCGAGCAGACGGGCATCCAGGGCATTGCTCCTTGGTGATGCTGCACCTCCTACAGCTTGG
TGTTTGGAAGCGGCACTGGGACGCTGCACTGACCAGTCTGCAGAAGGAACTGGAGGCTCCCCA
CCGAGGCTGGCTGCAGCTGCAGGAGGCCGACCTGTCGGGCCCTTCGACTCTTGGAGGCCCTGCT
GCAGACTGGGCCCCACCTGCTGCTTCAGACATATGTTTTTCTAGCCTCAGACTTCACAGATATT
GTGCCAGGGGTGAGCACCTGTTCCTGGTCCTCACTCTCCTGGGCACTGGTGTCTTACACT
CGCTTCATGGGCTTCATGAAGCCAGGCCACCTGGCCATGCCATGGGCCGCCCTCTTCTGCCAG
CAGCTCTGGAGGATGGGCATGTTGGGAACCCGCGTGCTGAGTCTGGTTCTGTTCTACAAAGCC
TACCACTTTTGGGTTTTTGTGGTTGCAGGTGCCCACTGGCTGGTGATGACATTCTGGCTTGTC
GCCCAGCAGAGTGACATCATCGACAGCACCTGCCACTGGAGGCTGTTCAACCTGCTCGTGGGG
GCCGTGTACATCCTCTGCTACCTCAGCTTCTGGGACAGCCCTTCTAGAAATAGGATGGTCACG
TTCTACATGGTCATGCTGTTGGAGAACATCATCCTGTTGCTGTTGGCCACCGACTTTCTCCAG
GGGGCATCGTGGACCAGCCTGCAGACCATAGCTGGGGTCCTGTCTGGATTTCTGATTGGCAGT
GTCTCACTGGTAATTTATTACAGCCTGCTGCATCCAAAATCCACAGACATCTGGCAGGGCTGC
CTAAGGAAGTCCTGTGGCATTGCAGGAGGTGATAAAACAGAGAGAAGAGATTCTCCCCGGGCC
ACAGATCTAGCTGGGAAGAGAACCAGAGCTCAGGCTCATGCCAAGGGGCAAGTTATGAACCA
ACCATTTTAGGGAAGCCCCCTACCCCTGAGCAGGTCCCCCAGAGGCTGGGCTGGGGACCCAG
GTTGCTGTGGAGGACTCTTTCCTCAGTCATCACCCTGGCTGTGGGTGAAACTTGCCCTAAAA
ACAGGAAATGTGTCTAAGATCAATGCCGCCCTTTGGAGATAACAGTCCTGCCTATTGTCCACCT
GCATGGGGGTTGAGTCAACAGGACTACCTGCAGAGAAAGGCCTTGTCTGCCAGCAAGAGCTC
CCATCCTCATCCCGTGACCCCTCAACCTTAGAGAACAGCTCTGCGTTTGAAGGTGTCCCTAAA
GCAGAGGCCGACCCATTGGAAACCTCAAGTTACGTATCTTTTGCCAGCGATCAGCAGGATGAA
GCACCTACCCAGAACCCAGCAGCCACGCAGGGGGAGGGCACCCCAAAGGAAGGAGCTGACGCT
GTTTCTGGGACACAGGGGAAGGGGACAGGTGGGCAGCAGAGAGGAGGGGAAGGACAGCAGAGT
TCCACGTTGTACTTCAGCGCCACTGCAGAAGTGGCCACATCCTCACAACAAGAAGGCAGCCCA
GCTACTCTGCAAACGGCCCACTCTGGAAGGAGGCTGGGAAAGAGCAGCCCTGCCAGCCTGCA
TCGCCCCACCCAGTGGGCTTGGCGCCCTTCCCCGACACCATGGCCGACATTAGCCCCATCCTA
GGCACAGGCCCATGTAGAGGCTTCTGCCCCAGTGCAGGCTTCCCTGGAAGAACCCTCAGTATC
TCAGAGCTAGAGGAGCCGCTGGAGCCCAAAGGGAGCTAAGTCACCATGCAGCTGTTGGTGTG
TGGGTGTCATTGCCACAGCTGAGGACTGCCCATGAGCCCTGCCTCACGTCCACCCCTAAGTCT
GAGTCTATCCAAACGGACTGCAGCTGCAGGGAACAGATGAAGCAAGAGCCGAGTTTTTTCATC
TGACCACAGTCATGGTGGGATAAGACAACAGGCTGACAAACCAAGCTGGCCATTTGGTACCGT
GAGAAAGGAAATCCCACTTCTGACACCTGTGTCCTTGGGCACATCACTGTCACCTCTGAATCT
CCATCTGCATCCCTGAAAAATGAAGAAACAGGGCTGGATGATTTTGCAGGTCCAATGCAAACA
TCACAGACCCACCCATGCATAGGAGAGACTCTAACATACTTTAGAGGAGGAGAAAGAGATTC
CAGTCAAAATTGTCTGCTACCTTTTATGAGCTGTAGGTTCCCTTATTTTATCTTTTGTCTGTG
GCTTCTAGGAAACACAAAGGTAAAACCCAGATTCTTATTTTATTTGAGGTTCTTGTTACAATT
AGCTTTGCCTCACATTTAGCGGTTATGAATCTCATTTTAAATATATTCTAACTGTATTATGTTA
TGAAATCTCTTGGTAAGATAATTTGCATGCTTTCTGGGAGTAGGTAAGGCCTGTGTGCTTGTA
ATAACTAACATAACTGAAAGTGCAAATGTCA

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FIGURE 524

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108726
><subunit 1 of 1, 686 aa, 1 stop
><MW: 74981, pI: 6.60, NX(S/T): 2
MHARLLGLSALLQAAEQSARLYTVAYYFTTGRLLWGWLALAVLLPGFLVQALSYLWFRAD
GHPGHCSLVMLHLLQLGVWKRHWDAALTSLQKELEAPHRGWLQLQEADLSALRLLEALLQ
TGPHLLLQTYVFLASDFTDIVPGVSTLFSWSSLSWALVSYTRFMGFMKPGHLAMPWAALF
CQQLWRMGMLGTRVLSLVLFYKAYHFWVFVAGAHWLVMTFWLVAAQQSDIIDSTCHWRLE
NLLVGAVYILCYLSFWDSPSRNRMVTFYVMMLLENIILLLLLATDFLQGASWTSLOTIAGV
LSGFLIGSVSLVIYYSLHHPKSTDIWQGCLRKSCGIAGGDKTERRDSPRATDLAGKRTE
SGSCQGASYEPTILGKPPTPEQVPPEAGLGTQVAVEDSFLSHHHWLWVKLALKTG NVSKI
NAAFGDN SPAYC PPAWGLSQQDYLQRKALSAQQELPSSSRDPSTLENSSAFEGVPKAEAD
PLETSSYVSFASDQQDEAPTQNPAATQGE GTPKEGADAVSGTQGKGTGGQQRGGEGQQSS
TLYFSATAEVATSSQQEGSPATLQTAHSGRRLGKSSPAQPASPHVGLAPFPDTMADISP
ILGTGPCRGEFCPSAGFPGRTLSISELEEPLEPKREL SHHAAVGVVWSLPQLRTAHEPCLT
STPKSESIQTDCSCREQMKQEPSFFI
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domains:

Amino acids 35-50;269-287;293-313

N-glycosylation sites:

Amino acids 416-420;467-471

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 344-348

N-myristoylation sites:Amino acids 188-194;288-294;299-305;335-341;338-344;362-368;
390-396;473-479;529-535;536-542;558-564;603-609;
643-649**Amidation sites:**

Amino acids 354-358;568-572

Leucine zipper pattern:

Amino acids 112-134

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FIGURE 525A

AGTGCCCTCTGTCATTTAATCTCCACGGAGTCCTGAAGGTGCTTCCCAGGTTTGTCCCCATCACACAGATGAGGC
AATCGTTCTGTTAAGACTGTCCTTGGGTCAATTAATGTCAGCAATGAAATCGGTGCTGCCATTACTAAACCTTACT
GTGTGCTGGCATTGTTGTATGCATGCATGTGTGTGCGTGCACACGTGTGTGTTTGCCTGTACATGTGCATGTGTGTG
TTGTGTGCCTGTGTGTGCACATGTAGAAAGAAAGTGATGTGTGGGAATGGAGAATTCCAACCCAGGAGGAGACTG
TGCCTGGGGCTGCCACGAGAAGTGGTGACACTTCGAGAAACGGGTTCCAAATGCACGTTGCCTTCCAGTTCTCTG
TGTGACCTTGGGCAAGTCACTTCAGCTCCCTGAGCTTTGTTTTTAAAAATATTTTTTAAATGTATAAAACCATGG
ACCATTACATATGAAGAGAAATGTGTGTGCAACATTCAAGTTAATAATCACAAGGTGGAGGAGTGCCTGCTCAGA
CCCAGAGCTGACACAGGGAACCTCTCCAGAAAGGCTGCAGGGCTTCCCTCCCAACCTCCAACGGCCCACTTGCTG
AGCCCGTGCTTATCTGTTCAAGTGGAAATGCCATGTGCCACGTTCCCTCAGAAGTAAAGCCACTAGGTAAGTGTGAC
ACTCTGTGCCAGCTTGGTGCAAGCCCCCTTGTGTGTGCTATCTTATTGACCTCCCAATAGCATGGTAAGGTCA
GTACTGTCACTTCCCCCACTTTGAAGATGAGGAGAGCACAAATTCATAGATGGAATGGAGGTCACGCAGTGGA
TAGGATCCAGACAGATTAATCCAATCTCAAGCCTGAATTCTTCCATTCCACGCTACGCTTGAAGCTCAATCTCTC
TTCCTGGTTGATTCTCCCCACTTCCCCACCCCAAGATATATCCCATCGCTGCTTGGTGGACAGTAGCCATGACTG
GGTTTTGGTAAAGGTTGCTGAATAATCAGGCTGCTGGTTAGTTTTTACATTTACCTTTCCAGTGAAATGGGGC
CCCATGAAAAAGGCAGCTCAAGTTGTAAATTAATCAAGGAAGGACAGAAAGGTCTTCTGTTTGCACCTACCCCTA
AGGATTTGGGGTAGACACTGGGAATTTACTAATTAATGAATTCAGTGCTTTCTTCTGCTGAAAGAGAGGCGTGGA
TCAACGCTGAGTGAAGGCATCAAGTTTAAGCTGCTAATTAATCTTCTGATCATGCAGATAAAAGCTACGTCCCTT
GAAATACACCAGGCAGCTAAACATAATCTTTGCGTTTCCGTAGTGTGGTTAAGGAATCCAGATGTTACTGCAAT
AACCCTCCATAAAACAAAGGAACACCCAGCTGTGAGAACTGGCTTCTCAGCATTCGTCCCAGCAGAGGCTCTTC
CGGGGCCAGCCCTGGAAGAACCCATCAGGGTTCTGATGGTTGCCCTGTTTCAGCACAGCCCTTATTGGCAGGCAG
ACGGCTACGGGCACAGCCACAGGCTGAAGGTGAGTCCAGCACACAACCTTTCTGACAGTGAACAGGAGTAAACATG
GGACCCACCCGAAACCTTTGTCTGTTGACTTCTTAGCAATGGAGGCAGCTCTAGGCTCTGGAGAGTTCCGGGTAT
AGGAGACCATGACTTGAGCAGACTGATATAAGTGGAATGCAAACATATTTAGATGGCACAACCTTAATTTAGATTT
ATCAGTGCTAATATAGAAAAAGCTAGTATTTATTGGGGCTTATTAGATTTTTAGTCTGAATCCTCACAACTTACG
AGGGGGTTCGTTTTACAGACTATGATCTTGCATGATTTCCCCAAAGATGCTCATTAAAGTATATGGTGAAAGTAGA
ATTTGAATACAGAAGACCTGGTTCTGCTACTTTCTGTGTTTCTATTTGGTTCAAACAGCCTTTCTTCTTTCAA
ACAACCTTCAGTGCAATTCATGGTTTTTGGAAAATAAACTTGATTTTGAGATTCAGACAATAAGTGCATTTTTAATG
TTTTATTCTTTTATCTTGA AAAACTGATATATTTATGAATGATATGTGCTCACTCAGTGTCAACACTTCAAACAA
CACAGACAGTACAATGACAAATTGGAGATCAGCTCTAATCTCGGCCCCCAATTTAATGCATTGCTGAATATTCTT
CTGAACATAGTCCATCCCACTGTCCCATGACACAAGACGCTCCAAGGGGCTGAAGATAGAGGGACTTCTGCAG
TCAAGAGAGCTGGGAACTCTTGGACAGTCACAATGTGCATTTGGGTATTAAAGGCTCTGCAAAGTTCTGCACCA
AATAAACCTTGGATTGGCTTGATCCAATGCCATGTTTCCAAAACCTACTTGCCCGTGGGACACCTTAGTCCATA
ACACAGGTGGCATTCTTCTAGAGAGTGTGCTGTGAAAAACACTGGTCTCACAGCACCGTGCATTTCATCCAGCA
GGTATTTACCAAGCAGGGACTTTGGGGCAGGTCCGTGCTAGGCTCTGCAGGTGGACCAGCCAGCCCTGACCTCCA
TGGTGTCTCTTCTCATGGGAGAGGCTGCACAGCAGTCATTGAGAAAACGAAGAAACACACAGGTACTTTCAGATG
CTGATAATGACTACCATGTGCTAAAAGAGCTCCAGGTGTTGTCTGTTTTGAGACAATCTTCTCGACAATGAGATA
GAATGAACCATGCAAACCTTGGGGGCTACGATGGTTTTAGGAAAGAGCTAGAGTGAAAAATCCTTTGACATATAT
ACATACAAATAAAGATACATGTGTATAATTTTATGTAATTGACATCACATTATATGCTGGCACCTGCCTTTTTTG
CTTAATGAAAATGTCAAAGGTAATATTACCAATCAATCAATATATTTACCATCGTGTTTAATTTCTGCAGAGCA
CTTATTCAAGCACATACTGCATTTTTCTTAGTCACTCACTGGTGGGAATAGAAAGTTTTCTCAGGCATGCATTTT
TCCCCTTCTGAAATGATCTCCTTAGAATAAATCCCCAAATTGATTGCTGGGTTCAAAGGCATGAACATTTTA
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GAAACATCTGTTCCCTATCCTTCGTCAATGTTCTCTTCATATGTTAACTTTTCTTATTGATTTGTTAGAGCACTT
TGTATATTGTGAATATTAGCTTTTGTGATCAGAATTATGGAATTGTTGTTGTCTTTAGTTTTGCTTATCAAGTTT
AAAGCCATTCAAGAGATGTTGTAAATGTGTATGTTGTAAATTTATGTCTTATTTTGTGTTTTCTGATGCTCATAT
GTTTAGAATGGTCAAGCAATCCCACTTATGATTACATAAATATCTCCCATATTTGCTCTTAGCATTTTTTTTC
TTTTCATGTAACCTTTGTTCTTTTCAAGGAATTTACTTTGCGGTAAGAAATGGGCTGGCTTCCAGTTTTATGTTTC
CCAAATGGTGATTCAAGCTGTTCCATTTCCATATTTCTCCCTTATTAGAAATGACCACTATATTATGTTCTAAAATA
TCTGCGTACTTGTGTCCCTTCCCTATAATCTCAGTTCATCTCTTTGAGCTATCTTTTGATTCTTTTTCAAACCAC
ACTGCTTTACTGAACTGTCATCATCTTATACATTTTTTAATACTCAGCAAGACAAGTTTCTCAATGCCACTCTTTT
TCAGAGTTTTTCTGGTGGTTGTAAGATGTTTATTCTTCTGGATAAACTTTAGAAATCACTCTTTTTGTCCAAGGTA
AAATATATCCACATTGAGATCATACTGAATATACAGACTAATTCAGGAAAAATGTATGTCTTTATTGCAATTGA
GTCTTCTTATCCAATAAAAAAGATATGAATTTCCATGTATTGAAATCTTCACTGAGACTTATTTTTGGCTTTTCA

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FIGURE 525B

CATGTCCTGCAAATGTATTGTTAAATTTATTTTATAGGTATTTTAGGGGAAATGATTTTCTAAAGTTTGTATTTTC
TAGCTTGTTATAATTTACATATGAGATAGTCATTGTTGTATATTATTTATAACTGATCATATTACTGTATTTGTA
TTGTTTTAATAGTTTTTCTATTATTTTGGGTTTTCCTGGAATACAACCTTATTATCTACAAATTATGATTGTTTT
GCCTTTTCCAATGTTTCATAACTGTTTTTATATTCTTGTCTGATTGCTTTGTTTCAGCACTTCTAGAATAAAGTCAT
GCAATACTAATGA

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FIGURE 526

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108728
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10922, pI: 8.81, NX(S/T): 0
MSAMKSVLPLLNPYCVLAFVYACMCVRAHVCVCVYMCMCVLCACVCTCRKKVMCGNGEFQ
PRRRLCLGLPREVVTLRETGSKCTLPSSSLCDLGQVTSAP

Important features of the protein:**Signal peptide:**

Amino acids 1-28

N-myristoylation sites:

Amino acids 80-86;94-100

Prokaryotic membrane lipoprotein lipid attachment sites:

Amino acids 13-24;34-45

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FIGURE 527

GTGAGACTTCTTTCTTCATTGTGGCTAGCTTTGAAAAGACCCTCTGAACTTCCTAAAGATATC
AAGATGATATCACCAGACTTGCCCTTTTTGACAATTGTCTTGATCATAGTTAGTTGGACAAC
TGTGGAGCACTAGCCATACTTCTTTCTTATCTTTACTATGTGTTTAAGGTTGTTTCATCTGCAA
GCCAGCTTAACAACCTTTTAAGAATAGCCAGCCTGTGAATCCCAAACACTCTAGAAGAAGTGAA
AAGAAATCCAATCATCATAAAGACTCCTCAATACACCATCTTCGTTTATCTGCCAACGATGCT
GAAGATAGCCTTCGCATGCACAGTACTGTGATTAACTTACTAACATGGATTGTATTACTCAGC
ATGCCTTCTCTAATTTATTGGCTAAAGAATCTTAGGTATTATTTTAAACTTAATCCTGATCCA
TGTAACCTTTGGCATTATCCTTATTCCGACTATGGCAATTCTTGGAATACTTACACTGTT
TCAATAAAATCAAGTAAATTGTTGAAGACTACTTCACAATTTCCACTTCCTCTGGCTGTTGGT
GTGATTGCTTTTGGGTCAGCACATTTATATAGGCTTCCATGCTTTGTCTTCATTCCTCTTTTA
CTCCATGCATTATGCAACTTTATGTAAGATTGGACTTAAGGAATGATGAAGATAATTTATGTG
TTTAGGGCCAGTGATAAGAGGGAACACACAGATCCATCAGTATGGACAGCAAGATCCTTTGGA
GAAGACAAGTCTATTTTTACAATATTGAAAATAGGAAATTAGTTTTGTAAATGTTTGAGGGAAG
TAGTTGAAGCATGGTTTTGTTTTGTGGTGTGGAATCCATGTACTAATCATTTTTGAAAAATTC
ATGAAGGGATATATGGTGATCACTATCATTGAGGACTCCTGTGCATATAAAATAGTCTGTTTT
ATCAACTGTAAA

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FIGURE 528

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108738
><subunit 1 of 1, 196 aa, 1 stop
><MW: 22225, pI: 9.90, NX(S/T): 0
MISPDLPFLTIVLIIVSWTTCGALAILLSYLYYVFKVVHLQASLTTFKNSQPVNPKHSRR
SEKKSNNHHKDSSIHHLRLSANDAEDSLRMHSTVINLLTWIVLLSMPSLIYWLKNLRYFFK
LNPDPCKPLAFILIPMAILGNTYTVSIKSSKLLKTTSQFPLPLAVGVIAFGSAHLYRLP
CFVFIPLLLHALCNFM

Important features of the protein:**Signal peptide:**

Amino acids 1-25

Transmembrane domains:

Amino acids 91-108;128-143;167-186

N-myristoylation site:

Amino acids 141-147

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FIGURE 529

GCGAGCCGGGTCCCACCA**ATG**GCCGCGAATTATTCCAGTACCAGTACCCGGAGAGAACATGTCA
AAGTTAAAACCAGCTCCCAGCCAGGCTTCCTGGAACGGCTGAGCGAGACCTCGGGTGGGATGT
TTGTGGGGCTCATGGCCTTCCTGCTCTCCTTCTACCTAATTTTCACCAATGAGGGCCGCGCAT
TGAAGACGGCAACCTCATTGGCTGAGGGGCTCTCGCTTGTGGTGTCTCCCGACAGCATCCACA
GTGTGGCTCCGGAGAATGAAGGAAGGCTGGTGCACATCATTGGCGCCTTACGGACATCCAAGCTT
TTGTCTGATCCAAACTATGGGGTCCATCTTCCGGCTGTGAAACTGCGGAGGCACGTGGAGATG
TACCAATGGGTAGAAACTGAGGAGTCCAGGGAGTACACCGAGGATGGGCAGGTGAAGAAGGAG
ACGAGGTATTCTACAACACTGAATGGAGGTGAGAAATCATCAACAGCAAAAACCTTCGACCGA
GAGATTGGCCACAAAACCCCAAGTGCATGGCAGTGGAGTCATTCATGGCAACAGCCCCCTTT
GTCCAAATTGGCAGGTTTTTCTCTCGTCAGGCCTCATCGACAAAGTCGACAACTTCAAGTCC
CTGAGCCTATCCAAGCTGGAGGACCCTCATGTGGACATCATTCGCCGTGGAGACTTTTTCTAC
CACAGCGAAAATCCCAAGTATCCAGAGGTGGGAGACTTGCGTGTCTCCTTTTCTATGCTGGA
CTGAGCGGCGATGACCCTGACCTGGGCCCAGCTCACGTGGTCACTGTGATTGCCCGGCAGCGG
GGTGACCAGCTAGTCCCATTCTCCACCAAGTCTGGGGATACCTTACTGCTCCTGCACCACGGG
GACTTCTCAGCAGAGGAGGTGTTTCATAGAGAACTAAGGAGCAACTCCATGAAGACCTGGGGC
CTGCGGGCAGCTGGCTGGATGGCCATGTTTCATGGGCCTCAACCTTATGACACGGATCCTCTAC
ACCTTGGTGGACTGGTTTTCTGTTTTCCGAGACCTGGTCAACATTGGCCTGAAAGCCTTTGCC
TTCTGTGTGGCCACCTCGCTGACCCTGCTGACCGTGGCGGCTGGCTGGCTCTTCTACCGACCC
CTGTGGGCCCTCCTCATTGCCGGCCTGGCCCTTGTGCCCATCCTTGTTGCTCGGACACGGGTG
CCAGCCAAAAGTTGGAG**TGA**AAAGACCCTGGCACCCGCCCGACACCTGCGTGAGCCCTGAGG
CTGGTTGTACAATGCCCACGCCTGCCTGGCTGCTTTCACCTGGGAGTGCTTTCGATGTGGGCA
CCTGGGCTTCCTAGGGCTGCTTCTGAGTGGTTCTTTCACGTGTTGTGTCCATAGCTTTAGTCT
TCCTAAATAAGATCCACCCACACCTAAGTCACAGAATTTCTAAGTTCCCCAACTACTCTCACA
CCCTTTTAAAGATAAAGTATGTTGTAACCAGGACGTCTTAAATGATTCTTTGTGTACCTTTTC
TGTCATATTCAGAAACCGTTCTGTGCCTGCTGGGAGTAATTCCTTTAGCAATTAAGTATTTGG
TAGCTGAATAAGGGGTCAGAACTTCTGAAACCAGAGATCTGTAATCATCTCTATTGGCCTGGG
GTGCCTGTGCTATAAATGAGTTTCTTCACATGAAAAACACAGCCAGCCCAAGATGACTTATCT
GGGTTTAGGATTCAATAGTATTCACCTAACTGCTTATTACATGAGCAATTTTCATCAAATCTCCA
AACTCTTAAAGGATGCTTTCGGAAAACACGCTGTATACCTAGATGATGACTAAATGCAAAATC
CTTGGGCTTTGGTTTTTTTTCTAGTAAGGATTTTAAATAACTGCCGACTTCAAAGTGTTCTTA
AAACGAAAGATAATGTTAAGAAAAATTTGAAAGCTTTGGAAAACCAAATTTGTAATATCATTG
TATTTTTTATTAAAAGTTTTGTAATAAATTTCTAAATTATCA

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FIGURE 530

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108743
><subunit 1 of 1, 400 aa, 1 stop
><MW: 44876, pI: 8.32, NX(S/T): 2
MAANYSSSTSTRREHVKVKTSSQPGFLERLSETSGGMFVGLMAFLLSFYLIIFTNEGRALKT
ATSLAEGLSLVVSPDSIHSVAPENEGRLVHIIGALRTSKLLSDPNYGVHLPVKLRRHVE
MYQWVETTESREYTEDGQVKKETRYSYNTEWRSEIINSKNFDREIGHKNPSAMAVESFMA
TAPFVQIGRFFELSSGLIDKVDNFKSLSLSKLEDPHVDIIRRGDFFYHSENPKYPEVGDLR
VSFSYAGLSGDDPDLGPAHVVTVIARQRGDQLVPFSTKSGDTLLLLHHGDFSAAEEVFHRE
LRSNSMKTWGLRAAGWMAMFMGLNLMTRILYTLVDWFPVFRDLVNIGLKAF AFCVATSLT
LLTVAAGWLFYRPLWALLIAGLALVPILVARTRVPAKKLE

Important features of the protein:**Transmembrane domains:**

Amino acids 34-53;365-388

N-glycosylation site:

Amino acids 4-8

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 140-144

Tyrosine kinase phosphorylation sites:

Amino acids 99-107;220-227

N-myristoylation sites:

Amino acids 35-41;93-99;310-316

Cell attachment sequences:

Amino acids 221-224;268-271

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FIGURE 531

AAAAAAAAAAAAAAAAAGAAGCTCTTATGCCAGGAACCTGGAATGGAGACCAAATATATATTG
GTTATATCATAGTATCACAGGGTTACTTTGGCATTGTTGGGAACTTGAGAGAAATGGGCAATAA
CTGTTACTTTAAAAGCTTGGGTGCTGTGATTCTGCCTTCAGCCTCAGCCACTTTTGTGGTGCT
TTGCGTGGCATCAGTACCTCCACTGATTCTTCTGTCTTTCCTCTCTCTCTTCCCCCCTCTTT
CCCTTCTGTTTTTCTCAGATCTAAGGGTTATAATGGAGGGGCAAACCTGCCTGGCTATTTCAGA
TAAGACTTCACTGAGTGACTGTTTCAGCCCATGATTTACCCTGCAGTTTAACAGGCTCAGGAAT
TAGGTCGCATCAGTTGAGCGCGGGTCACTTAGGCCTATAATCATCATCAGACGGCAATTAAAG
GACCATTCTGCCTTTTTTCACTATTACATCCCCCGCCTGTAGCCAGCCTGCCATACAGTAGA
TACTCAATAAATATTTGCTGAATGATAACCAATAA

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FIGURE 532

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108758
<subunit 1 of 1, 100 aa, 1 stop
<MW: 10316, pI: 8.52, NX(S/T): 0
MGNNCYFKSLGAVILPSASATFVVL CVASVPPLILLSFLSLFPPSFPSVFLRSKGYNGGA
NCLAISDKTSLSDCSAHDLPCLTGS GIRSHQLSAGHLGL

Important features of the protein:**Signal peptide:**

Amino acids 1-47

N-myristoylation site:

Amino acids 58-64

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FIGURE 533

CGGGGTGTACGAAAGAGAAACCCGGAGGGCGCCGGGGACTGGGCCGGGGTCTGCAGGGCTCAG
CTGAGCCCATGAGCTCCCAGAGCTAACCCCTGAACACCCAGGCGGGCAAAGGGCTGATGTCGG
TAGTCCCATCCTGGAGGGGCAGGCTCTGCGCATCTGCTCCTGGCATGGCGCTGCGGCACCTC
GCCCTCCTGGCTGGCCTTCTCGTGGGAGTCGCCAGCAAGTCCATGGAGAACACGGCCCAGCTG
CCCGAGTGCTGTGTGGATGTGGTGGGCGTCAACGCCAGCTGCCAGGCGCAAGTCTGTGTGGT
CCAGGCTGTTACAGGCGCTGGAACGCGGACGGGAGCGCCAGCTGCGTCCGCTGTGGGAACGGA
ACCCTCCCAGCCTACAACGGCTCCGAGTGTAGAAGCTTTGCTGGCCCCGGGTGCGCCATTCCCC
ATGAACAGAAGCTCAGGGACCCCCGGGCGGCCACATCCTGGGGCTCCGCGCGTGGCCGCCTCC
CTCTTCCTGGGCACGTTCTTCATTAGCTCCGGCCTCATCCTCTCCGTAGCTGGGTTCTTCTAC
CTCAAGCGCTCCAGTAAACTCCCCAGGGCCTGCTACAGAAGAAACAAAGCTCCGGCCCTGCAG
CCTGGCGAAGCCGCTGCAATGATCCCCCGCCACAGTCCTCAGACGTGGGGTCTGCAGGAAAG
GAGGACCCACCACGACAGGGCAGACCCCCAATACCTGCTCCTCCTTGAAGTCCAGCTCCACCC
GAGGACAGACGCAGCCGGCCTCCGCCAGGCCCTCCTGAGCAGCCATCGCTTCAGTGGTGCTGG
GTCAGGCGGACCCAAGAGTCAGCCCGTACGGAAGCCGCGCTACGTGAGGCGGGAGCGGCCCT
GGACAGGGCCACGGATCCCGCTGCCTTCCCGGGGGAGGCCCGTATCAGCAATGTCTGACCTGG
AGGCCGAGACCACGCCACGCACTTGGCGGCAGGGACCCGGAGGCCGACCCCTTGGCGGGAACC
AGCACAAAGTGTTGGCATCGCCCGGCGCCCGGGACAGTCCTGGGCACAGCCTCGGCTCTGGGT
CCCTCCGCCTCCCAGCGACGGACGCCAAAGGGTCCCGGGCCGCCTGAGGCTCCTCCCCACCAC
AGCCATCTCGTTTATCGGACCAGGAGCAGGCATCCATGAGACCTCAGAGCTTCAGATCGAGGC
CTTGGGGGGTCCGGGCCCCCCCCAGGAAACACGGTGAGGCCCCAGCGCCTGCAGCCAAAGCTGG
CACGATCTATGGGGCAGGTGCCGCTCTGCCTAGAAAAGCCAGGGGCTCTGCTGCCGTGCCCTC
CAGAGCCCACAGCGGGCAGGACTCCTCCAGCACACCACACCCAGTGGCCCCGAGACCCCTCTG
AGAACAGTGAGGCTGGTCCTCGTGCCGTTCCAGCCGGTGCCCGGCCAGTGGGGAGGACACAGC
CTAGGAACCAGCTGCCTGAGACCAGGGTGCCCTCTGGGCTGTCCTCCCGCGTGGCGGAGACCCC
AAGCACGCAGCCACCCATTTCCGGAGCTGCAGGATAGAGCTTCCTCTTGATCTCTGTTTTTAAG
CAGAAATTCAATTGTGCAGAAAAGTCCTCCAGAGCTCTGTGGCCCCGCTCGGATCCGCTGGACC
CCCATGCCTGGCTGATCCCTGCCACGTGGGGCAGGCCACATCTAACCCCCACAAGTCACTG
CCTCACTGCACCTGCCAAGGCTGCCCTGGCGCTGAGTCCTGGGGTCCCTCCCGGAGTTCCTGG
GAGAAAGGCGCCGTCGTGGCCGCCTCCCGCACGCCAGGCCCGGGCTCCACCGTGGGTCTCAGA
CGCCCTGCGGCACCGGCACCGTCTGCTTTAGCATGGGACCCCCATCTGAGGGGTGGCCTGGCC
TTCGGGGTCCCCACGCTCCTTTGCGAAGTCCACTGTGGGTGCCATCATGGTCTCCGGGACCTG
GGCCAGCGGGAACGTGGGGGCACTGGGTGTGCTGATATAAAGTCGGCATTACTCAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 534

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108765
><subunit 1 of 1, 189 aa, 1 stop
><MW: 19464, pI: 9.60, NX(S/T): 4
MALRHLALLAGLLVGVASKSMентаQLPECCVDVVGVNASCPGASLCGP GCYRRWNADGS
ASCVRCGNGTLPAYNGSECRSFAGPGAPFFPMNRSSGTPGRPHPGAPRVAASLFLGTFFIS
SGLILSVAGFFYLKRSSKLPRACYRRNKAPALQPGEAAAMIPPPQSSDVGSAGKEDPPRQ
GRPPI PAPP

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 111-129

N-glycosylation sites:

Amino acids 38-42;68-72;75-79;92-96

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 134-138

N-myristoylation sites:

Amino acids 11-17;36-42;43-49;59-65;69-75;122-128

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FIGURE 535

TGGATCTGCGGGAATGTGGGCTGGAGAGGTCCTGCCGTGGTACCAGCCTCCAGCCTGCCCCCA
GGACTGCCCCCTGACCCAGGCGCGCCCGCTGCTCGGTGGCAGGAGGGCCGGCGGAGCGCC**ATGG**
CCTGCATCCTGAAGAGAAAGTCTGTGATTGCTGTGAGCTTCATAGCAGCGTTCCTTTTCCTGC
TGGTTGTGCGTCTTGTAAATGAAGTGAATTTCCCATTTGCTACTAACTGCTTTGGACAACCTG
GTACAAAGTGGATAACCATTTCTCCTACACATACAGGCGGCCCCCTTCGAACTCACTATGGATACA
TAAATGTGAAGACACAAGAGCCTTTGCAACTGGACTGTGACCTTTGTGCCATAGTGTCAAACCT
CAGGTCAGATGGTTGGCCAGAAGGTGGGAAATGAGATAGATCGATCCTCCTGCATTTGGAGAA
TGAACAATGCCCCCACCAAAGGTTATGAAGAAGATGTCGGCCGCATGACCATGATTCGAGTTG
TGTCCCATACCAGCGTTCCTCTTTTGCTAAAAAACCTGATTATTTTTTCAAGGAAGCGAATA
CTACTATTTATGTTATTTGGGGACCTTTCCGCAATATGAGGAAAGATGGCAATGGCATCGTTT
ACAACATGTTGAAAAAGACAGTTGGTATCTATCCGAATGCCCAAATATACGTGACCACAGAGA
AGCGCATGAGTTACTGTGATGGAGTTTTTAAGAAGGAACTGGGAAGGACAGTACAGAG**TGAC**
CATGCAGTGTTGATTGATCGAACAGCAACCACCACATACATGTCCTGCCCCACCACAAAAGGA
AGGAAGGAATAAAAGAAAGAAAGAAAGAAACAAACAAACAAACAAACAAACTAAGCAAGACA
AAACAAATACCCATGTCAGTGGTTCAAAGATTAAGATTGTGGCTTTGTGTAAAGTTCTTTCCC
TTTGTAGACTTGCTGCATAATTATTCAGGTATGATGGTTACAGTTTTTAAAAAGGAAGGGAAA
TTGTGGTATGTGGTATGTAAATATTTTTTAAATGTTGTCTCTCTGTTTTGATCAGTTTTTGTTT
TATTCAATTTGTCTTTATTAAATCTTATCAAAGCA

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FIGURE 536

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108783
><subunit 1 of 1, 210 aa, 1 stop
><MW: 24022, pI: 9.51, NX(S/T): 1
MACILKRKSVIAVSFIAAFLLVRLVNEVNFPLLLNCFGQPGTKWIPFSYTYRRPLRT
HYGYINVKTQEPLQLDCDLCAIVSNSGQMVGQKVGNEIDRSSCIWRMNNAPTKGYEEDVG
RMTMIRVVSHTSVPLLLKNPDYFFKEANTTIYVIWGPFRNMRKDGNGIVYNMLKKTVGIIY
PNAQIYVTTEKRMSYCDGVFKKETGKDSTE

Important features of the protein:**Signal peptide:**

Amino acids 1-27

N-glycosylation sites:

Amino acids 148-152

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 6-10;191-195;201-205

N-myristoylation sites:

Amino acids 41-47;87-93;91-97;167-173;178-184

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FIGURE 537

GTTTTATTGACAATACATGCATCATATCTTTTGACTTTGAAGGATATCTCATGTCAAAGGAAT
CAAGTTATGATTTATAGAGGATTCAGCTGGAATACCTTGTGGGTGCTGGCTGAGGGTGGCAAA
ACGCCTACCGAGACATGAAGGTTTTAGCCACTAGTTTTTGTCTTGGGAGCCTGGGGTTGGCCT
TCTACCTGCCTTTGGTGGTGACTACACCTAAAACACTGGCCATCCCTGAGAAGCTGCAAGAAG
CTGTGGGGAAAGTTATCATCAATGCCACAACCTGTACTGTCACCTGTGGCCTTGGCTATAAGG
AGGAGACCGTCTGTGAGGTGGGCCCTGATGGAGTGAGAAGGAAATGTCAGACTCAGCGCTTAGAA
TGTCTGACCAACTGGATCTGTGGGATGCTCCATTTACCATTCTCATTGGCAAGGAATTTGAG
CTTAGCTGTCTGAGTTCAGACATCTTGGAGTTTGGACAGGAAGCTTTCCGGTTCACCTGGAGA
CTTGCTCGAGGTGTCATCTCCACTGACGATGAGGTCTTCAAACCCTTTCAAGCCAACTCCAC
TTTGTGAAGTTTAAATATGCTCAGGAGTATGACTCTGGGACATATCGCTGTGATGTGCAGCTG
GTAAAAAACTTGAGACTTGTCAAGAGGCTCTATTTTGGGTTGAGGGTCCTTCCTCCTAACTTG
GTGAATCTGAATTTCCATCAGTCACTTACTGAGGATCAGAAGTTAATAGATGAGGGATTGGAA
GTTAATCTGGACAGCTACTCCAAGCCTCACCACCCAAAGTGGAAGAAAGGTGGCGTCAGCC
TTGGGAATAGGAATTGCCATTGGAGTGGTTGGTGGCGTGTGGTGAGGATTGTCCTCTGTGCG
CTAAGGGGGGGCCTGCAGCAGTGACAGCTTCAAGAACTTAACAGCCTTGCTCCTGAAGAACTG
GCTGCCCAGGAAGCCAAGCTAGCTTTTTAGGGGAGTGTTCCAGCTGCTGGTAGTGGATCAGCT
TAGAGGGAACACTCCCACAGCCAAAAGAATGAGTGGGAGAAATGGAGGGGACAATCTCCTGGG
AGCTATGCGCAGTAACCTAACTTCCTTATGTCCCATGGATCTCTTCCTGATCTTCCCTGCCCA
TTGGGTACCCAGGAACTGCAAGCATTGCCTGTGTTCTGGAAGAGTTCTAAGAAGCTTGCA
TTCATTTTCTACCCTTTATGACTTGGATGCCTCCCCACCTCCATTTCCCCTCTTCTGAGCTGT
GTATTCATGTAGAGGGATGTATTCAGCCTTTTTAGTGAACATTTTTTTTCAATAAAAGTAATT
CACAGTAA

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FIGURE 538

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108789
><subunit 1 of 1, 255 aa, 1 stop
><MW: 28440, pI: 8.92, NX(S/T): 1
MKVLATSFVLGSLGLAFYLPVVTPKTLAIPEKLQEAVGKVIINATTCTVTCGLGYKEE
TVCEVGPDGVRRCQTORLECLTNWICGMLHFTILIGKEFELSCLSSDILEFGQEAFT
WRLARGVISTDDEVFKPFQANSHFVKFYAQEYDSGTYRCDVQLVKNLRLVKRLYFGLRV
LPPNLVNLNFHQSLTEDQKLIDEGLEVNLDSSKPHHPKWKKKVASALGIGIAIGVVGGV
LVRIVLCALRGGLQQ

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 225-244

N-glycosylation site:

Amino acids 45-49

N-myristoylation sites:

Amino acids 126-132;156-162;204-210;229-235;231-237;235-241

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FIGURE 539

GCGCTCATCACTGGCTGGGGACAGAGCCGGGCACCAAGGAGCGACAGGATCCCGAAGAGAGAG
AGAGAAGGCAGCGAGGGAAGGAGGACCCCGGCAGGCAGCAGC**ATG**AAATTCAGCCCAGCGCAC
TACCTGCTGCCTCTCCTGCCTGCGCTGGTCCTCAGCACCCAGACAGGACTATGAAGAGCTAGAA
AAGCAGCTGAAAGAAGTCTTTAAGGAGCGAAGCACCATTTCTTCGTCAGCTGACAAAGACATCA
AGAGAACTTGATGGAATTAAAGTCAATCTTCAGTCCTTAAAAAACGATGAGCAGTCTGCCAAA
ACTGATGTTTCAGAACTTCTGGAATTAGGACAGAAACAAAGAGAAGAAATGAAGTCTCTTCAG
GAGGCCCTGCAAAATCAGCTTAAGGAGACATCAGAGAAAGCAGAAAAACACCAGGCTACTATT
AATTTTTTAAAGACTGAAGTTGAAAGAAAGAGCAAAATGATCCGAGACCTCCAGAATGAGGAT
TCAAGGAAGAGACCAAGAGATCTCCAGTGGAAGATAGTCTCCATGAGGACCATGTCAATATAC
TTATTGATGTATCTC**TAG**TACCTAGAATAGTGGAGATTTATATTAGATACAAAATAAATATGT
GTGGAATTAATTAATAA

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FIGURE 540

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108806
><subunit 1 of 1, 159 aa, 1 stop
><MW: 18865, pI: 9.76, NX(S/T): 0
MKFSPAHYLLPLLPAVLSTRQDYEELEKQLKEVFKERSTILRQLTKTSRELDGIKVNLO
SLKNDEQSAKTDVQKLLELGQKQREEMKSLQEALQNQLKETSEKAEKHQATINFLKTEVE
RKSKMIRDLQNEQSRKRPRDLQWKIVSMRTMSIYLLMYL

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation site:

Amino acids 54-60

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FIGURE 541

CTCCACGAGGCTGCCGGCTTAGGACCCCCAGCTCCGACATGTCGCCCTCTGGTCGCCTGTGTC
TTCTCACCATCGTTGGCCTGATTCTCCCCACCAGAGGACAGACGTTGAAAGATAACCACGTCCA
GTTCTTCAGCAGACTCAACTATCATGGACATTTCAGGTCCCGACACGAGCCCCAGATGCAGTCT
ACACAGAACTCCAGCCCACCTCTCCAACCCCAACCTGGCCTGCTGATGAAACACCACAACCCC
AGACCCAGACCCAGCAACTGGAAGGAACGGATGGGCCTCTAGTGACAGATCCAGAGACACACA
AGAGCACCAAAGCAGCTCATCCCCTGATGACACCACGACGCTCTCTGAGAGACCATCCCCAA
GCACAGACGTCCAGACAGACCCCCAGACCCTCAAGCCATCTGGTTTTTCATGAGGATGACCCCT
TCTTCTATGATGAACACACCCTCCGGAAACGGGGGCTGTTGGTCGCAGCTGTGCTGTTTCATCA
CAGGCATCATCATCCTCACCAGTGGCAAGTGCAGGCAGCTGTCCCGGTTATGCCGGAATCGTT
GCAGGTGAGTCCATCAGAAACAGGAGCTGACAACCTGCTGGGCACCCGAAGACCAAGCCCCCT
GCCAGCTCACCGTGCCCAGCCTCCTGCATCCCCTCGAAGAGCCTGGCCAGAGAGGGAAGACAC
AGATGATGAAGCTGGAGCCAGGGCTGCCGGTCCGAGTCTCCTACCTCCCCCAACCCTGCCCCGCC
CTGAAGGCTACCTGGCGCCTTGGGGGCTGTCCCTCAAGTTATCTCCTCTGCTAAGACAAAAAG
TAAAGCACTGTGGTCTTTAAAAA
AAAAAAAAAAAAAAAAAAAAA

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FIGURE 542

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108936
><subunit 1 of 1, 178 aa, 1 stop
><MW: 19472, pI: 5.71, NX(S/T): 0
MSPSGRLCLLTIVGLILPTRGQTLKDTTSSSSADSTIMDIQVPTRAPDAVYTELQPTSPT
PTWPADETPQPQTQTQOLEGTDGPLVTDPEETHKSTKAAHPTDDTTLSERPSPSTDVQTD
PQTLKPSGFHEDDPFFYDEHTLRKRGLLVAAVLFITGIIILTSKGKCRQLSRLCRNRCR

Important features of the protein:**Signal peptide:**

Amino acids 1-21

Transmembrane domain:

Amino acids 147-162

Tyrosine kinase phosphorylation site:

Amino acids 45-52

N-myristoylation site:

Amino acids 146-152

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FIGURE 543

CGGCTCGAGGTGAGAAGGAACTGCAAGAGTGGGGCAGAGAACCAGAGTGTGAGAGCAAAACC
TCCTCTATCTGCACATCCTGGGGACGAACCGGGCAGCCGGAGAGCTGCGGCCGGCCCAGTCCC
GCTCCGCCTTTGAAGGGTAAAACCCAAGGCGGGGCCTTGGTTCTGGCAGAAGGGACGCT**ATGA**
CCGCAGAATTCTCTCCCTGCTTTGCCTCGGGCTGTGTCTGGGCTACGAAGATGAGAAAAAGA
ATGAGAAACCGCCCAAGCCCTCCCTCCACGCCTGGCCCAGCTCGGTGGTTGAAGCCGAGAGCA
ATGTGACCCTGAAGTGTGAGGCTCATTCACAGAATGTGACATTTGTGCTGCGCAAGGTGAACG
ACTCTGGGTACAAGCAGGAACAGAGCTCGGCAGAAAACGAAGCTGAATTCCCCTTCACGGACC
TGAAGCCTAAGGATGCTGGGAGGTACTTTTGTGCCTACAAGACAACAGCCTCCCATGAGTGGT
CAGAAAGCAGTGAACACTTGCAGCTGGTGGTCACAGATAAACACGATGAACTTGAAGCTCCCT
CAATGAAAACAGACACCAGAACCATCTTTGTCGCCATCTTCAGCTGCATCTCCATCCTTCTCC
TCTTCCTCTCAGTCTTCATCATCTACAGATGCAGCCAGCACGGTTCATCATCTGAGGAATCCA
CCAAGAGAACCAGCCATTCCAACTTCCGGAGCARGAGGCTGCCGAGGCAGATTTATCCAATA
TGGAAGGGTATCTCTCTCGACGGCAGACCCCCAAGGAGTGACCTATGCTGAGCTAAGCACCA
GCGCCCTGTCTGAGGCAGCTTCAGACACCACCCAGGAGCCCCCAGGATCTCATGAATATGCGG
CACTGAAAGT**GTAG**CAAGAAGACAGCCCTGGCCACTAAAGGAGGGGGGATCGTGCTGGCCAAG
GTTATCGGAAATCTGGAGATGCAGATACTGTGTTTCCTTGCTCTTCGTCCATATCAATAAAAT
TAAGTTTCTCGTCTTA

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FIGURE 544

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119510
><subunit 1 of 1, 236 aa, 1 stop
><MW: 26079, pI: 5.05, NX(S/T): 3
MTAEFLSLLCLGLCLGYEDEKKNEKPPKPSLHAWPSSVVEAESNVTCLKQAHSQNVTFVL
RKVNDSGYKQEQSSAENEAEFPFTDLKPKDAGRYFCAYKTTASHEWSESSEHLQLVVTDK
HDELEAPSMKTDTRTIFVAIFSCISILLFLSVFIIYRCSQHGSSEESTKRTSHSKLPE
QEAAEADLSNMERVSLSTADPQGVTYAELSTSALSEAASDTTQEPPGSHEYAALKV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-16

Transmembrane domain:

Amino acids 135-153

N-glycosylation sites:

Amino acids 44-48;55-59;64-68

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 171-175

Tyrosine kinase phosphorylation sites:

Amino acids 61-69;87-95

N-myristoylation sites:

Amino acids 12-18;203-209

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FIGURE 545

GGCGGCCCGGAGCTGGGAGCGCGGGGAAGGCGGTTGGGGTTCTGACAGCTGCGCGCGATCCTG
CTCTCTCTCAGCCGCCTGTGGACATGCGCAAAGGGCCCTCTCCTGAGTCCAGATGATGCTCAT
ACCAATGGCTTCAGTGATGGCGGTGACTGAACCGAAATGGGTCTCGGTCTGGAGCCGCTTCCT
CTGGGTGACGCTGCTGAGCATGGTGCTGGGGTCCCTGCTGGCCCTGCTGCTGCCGCTGGGGGC
TGTGGAGGAGCAGTGCTTGGCTGTGCTCAAAGGCCTCTACCTGCTCAGGAGCAAACCGGACAG
GGCGCAGCATGCCGCCACCAAGTGCACCAGCCCGTCCACGGAGCTCAGCATCACCTCCAGGGG
CGCGACGCTGCTGGTGGCCAAGACCAAGGCCTCTCCAGCGGGTAAGTTGGAAGCCAGAGCTGC
CCTGAACCAGGCCCTGGAGATGAAGCGCCAGGGCAAGCGGGAAAAAGCCCAAAGCTCTTCAT
GCACGCCCTCAAGATGGACCCGGACTTCGTGGACGCGCTCACCGAGTTTGGCATCTTCTCGGA
AGAAGACAAGGACATCATCCAGGCGGACTACTTGTACACCAGAGCATTGACCATCTCACCTA
CCATGAGAAAGCACTGGTCAACCGCGATCGGACACTGCCTCTTGTGGAAGAGATCGACCAGAG
GTATTTTCAGCATCATCGACAGCAAAGTGAAGAAGGTCATGTCCATCCCCAAGGGGAAGTCAAGC
TCTGCGCAGGGTCATGGAGGAGACCTACTACCATCACATCTACCACACAGTGGCCATCGAGGG
CAACACCCTCACCTCTCGGAAATCAGGCACATCCTGGAGACCCGCTACGCCGTGCCCGGGAA
GAGCCTGGAGGAGCAGAACGAGGTCATAGGCATGCATGCAGCCATGAAGTACATCAACACGAC
TCTGGTTTCGCGCATCGGCTCCGTACCATCAGCGACGTGCTGGAGATCCACAGGCGGGTGCT
GGGCTACGTGGACCCCGTGGAAGCCGGCAGGTTTCGGACAACACAGGTCCTGGTTCGGACACCA
CATCCCTCCCCATCCGCAGGATGTGGAAAAGCAGATGCAGGAGTTTGTACAGTGGCTCAACTCC
GAGGAAGCCATGAACCTGCACCCAGTGGAGTTTGCAGCCTTAGCCCATTTATAAAGTTCGTTTAC
ATCCACCCTTTTCATTGATGGCAACGGGAGGACCTCCCGTCTGCTCATGAACCTCATCCTCATG
CAGGCGGGCTACCCGCCCATCACCATCCGCAAGGAGCAGCGGTCCGACTACTACCACGTGTTG
GAAGCTGCCAACGAGGGCGACGTGAGGCCTTTCATTTCGCTTCATCGCCAAGTGTACTGAGACC
ACCCTGGACACCCTGCTTTTTGCCACAACTGAGTACTCGGTGGCACTGCCAGAAGCCCAACCC
AACCCTCTGGGTTCAAGGAGACGCTTCCTGTGAAGCCCTAACCCTAGAAATCCTCAGTGACA
AAGGCTGTCCTGAGGTAGGAAA

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FIGURE 546

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119517
><subunit 1 of 1, 458 aa, 1 stop
><MW: 51778, pI: 7.81; NX(S/T): 2
MMLIPMASVMAVTEPKWVSVWSRFLWVTLLSMVLGSLALLPLGAVEEQCLAVLKGLYL
LRSKPDRAQHAATKCTSPSTELSITSRGATLLVAKTKASPAGKLEARAALNQALEMKRQG
KREKAQKLFMHALKMDPDFVDALTEFGIFSEEDKDIIQADYLYTRALTISPYHEKALVNR
DRTLPLVEEIDQRYFSIIDSQVKKVMSIPKGNSALRRVMEETYHHIYHTVAIEGNTLTL
SEIRHILETRYAVPGKSLEEQNEVIGMHAAMKYINTTLVSRIGSVTISDVLEIHRRVLGY
VDPVEAGRFRRTTQVLVGHHIPHPQDVEKQMDEFVQWLNSEEAMNLHPVEFAALAHYKLV
YIHPFIDGNGRTSRLLMNLILMQAGYPPITIRKEQRSDDYHVLEAANECDVRPFIRFIAK
CTETTLDTLLFATTEYSVALPEAQPNSHSGFKETLPVKP

Important features of the protein:**Signal peptide:**

Amino acids 1-46

N-glycosylation sites:

Amino acids 275-279;446-450

Tyrosine kinase phosphorylation sites:

Amino acids 216-225;217-225;244-232

N-myristoylation sites:

Amino acids 35-41;235-241;266-272;368-374

Amidation site:

Amino acids 119-123

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FIGURE 547

CCTCTGTCTGTGCTCCCATCCCAGGGAGTATAGGTGGAGCCTCCAGAGCCCATGGACAGGGCA
TGCTGGGGCTGGGCCAGCCCCAGCGGTGTCTCTAAGGCACCCCTGGGATCCCCACTGAGCTGG
CCTACTTCAGACAGCCAGGGCCCCACCCCTCTGGCCCCCTTAGTGTCCAGCTCGTGGCCCCCTTG
GCATTTCCACAAGACGCCAAGATGGAGATTCCCATGGGGACCCAGGGCTGCTTCTCAAAGAGC
CTCCTGCTCTCAGCCTCAATCCTGGTCCTCTGGATGCTCCAAGGCTCCCAGGCAGCTCTCTAC
ATCCAGAAGATTCCAGAGCAGCCTCAAAAGAACCAGGACCTTCTCCTGTGAGTCCAGGGTGTG
CCAGACACCTTCCAGGACTTCAACTGGTACCTGGGGGAGGAGACGTACGGAGGCACGAGGCTA
TTTACCTACATCCCTGGGATACAACGGCCTCAGAGGGATGGCAGTGCCATGGGACAGCGAGAC
ATCGTGGGCTTCCCCAATGGTTCCATGCTGCTGCGCCGCGCCCAGCCTACAGACAGTGGCACC
TACCAAGTAGCCATTACCATCAACTCTGAATGGACTATGAAGGCCAAGACTGAGGTCCAGGTA
GCTGAAAAGAATAAGGAGCTGCCCAGTACACACCTGCCACCAACGCTGGGATCCTGGCGGCC
ACCATCATTGGATCTCTTGCTGCCGGGGCCCTTCTCATCAGCTGCATTGCCTATCTCCTGGTG
ACAAGGAAGTGGAGGGGGCCAGAGCCACAGACTGCCTGCTCCGAGGGGGCCAGGGATCTCTGTCC
ATCTTGTGCTCGGCTGTATCCCCAGTGCCTTCAGTGACGCCCAGCACATGGATGGCGACCACA
GAGAAGCCAGAATTGGGCCCTGCTCATGATGCTGGTGACAACAACATCTATGAAGTGATGCCC
TCTCCAGTCCTCCTGGTGTCCCCCATCAGTGACACAAGGTCCATAAACCCAGCCCGGCCCTG
CCCACACCCCCACACCTGCAGGCGGAGCCAGAGAACCACCAAGTACCAGCAGGACCTGCTAAAC
CCCGACCCTGCCCCCTACTGCCAGCTGGTGCCAACTTCTTGATGGGTCTCTGGGCCAGGCCAGC
CAGGGAGAAGACAAGGCCCCAGCCCTCCTCTGGGAGCCTCACACCTGAGACCAGCAGGACAAG
GCCATTGGGGGGCTGTGGGGCCGATGAGGTGGACTCAGCCAAAGACTCAGCAGCACATGGGGCA
GGTGTCTTGGCAGGGGGACAGGAGACTGTAACAGGCCCAGGTCCTTGTGCAGCCCCTGAATGC
ACGCCCCGCTTCGGTCTGTTCTTCAAGCAAGCTGGCCTGGGCCATGTGCCTGTGAAAGGCAG
GCTCTGGCCCCCTTTCATGCCAAAGTCCCCCAAGATCTGGATATCTGGGGACAAGATGGTGGC
CTCAGGCCTGCCTCCCAGGCAGTTGGCTGGGCTCCCAACTGTCTGTCTCAATGCCCTACCCC
AACTCCACTAGTGACCCTCAGAGTCTTCTCCCCCTTAGGACAAGGCAGACACCCCACCATGCGG
GCCTCAGGTGGCAGAGAGGCCAGCCTCACAGGCCTGTGGCCCCACACACCAGTCCCAGCAAG
GTGACCACGGCTGCTGGACCCCTTCCCTGTTTCAGGCAGGCCCAGCCCCTCTCAGAACCTGCTG
CCAGCTGCTGGTCTTGGCCCCCACCCTGAATCTTACTGAGTCCCTCTGGGCAGCAGCTCCCTT
CTCCACCCCACCCCAGCACCCGTCCCAAATGTGGCCTCAGCTTGTCTCTCCCTTCCCCAAACT
ATGCATTCATTCAGCAATAAATGAGCCTTTGCTGCA

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FIGURE 548

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119535
><subunit 1 of 1, 300 aa, 1 stop
><MW: 32638, pI: 6.02, NX(S/T): 1
MEIPMGTOGCFSKSLLLSASILVLWMLQGSQAALYIQKIPEQPQKNQDLLLSVQGVPDF
QDFNWYLGEETYGGTRLFTYIPGIQRPQRDGSAMGQRDIVGFPNGSMLLRRAQPTDSGT
QVAITINSEWTMKAKTEVQVAEKNKELPSTHLPTNAGILAATTIIGSLAAGALLISCIAYL
LVTRNWRGQSHRLPAPRGQGSLSILCSAVSPVPSVTPSTWMATTEKPELGPAGHDAGDNNI
YEVMPSPVLLVSPISDTRSINPARPLPTPPHLQAEPENHQYQQDLLNPDPAPYCQLVPTS

Important features of the protein:**Signal peptide:**

Amino acids 1-32

Transmembrane domain:

Amino acids 159-178

N-glycosylation site:

Amino acids 104-108

N-myristoylation sites:

Amino acids 6-12;29-35;55-61;91-97;157-163;165-171

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FIGURE 549

GCCACTCACACCATCTGCTAATGGGACAGCTCACTCTTCCCTCCAAACCATGGCCTTGGCTCA
AGAGCTTCCTTGTTTCTGGAATGTTCTTTCCTCCAGCTCCAGGTGTTGAAATTCTGCCTGGTC
TGGGTCTCCTGTTGAAGGACGCCCTCCACTGGGAAGGATCCTCTTGCCCTCACCACCTTGCTTT
CACCAGCCCCCTGCTCCCCCTCTTCTCTTGGGGCTGTTGTCGTTGTTGATACTTTTTTTTTTGT
GTGTTTGACACACATCTTCTTCTCACCCCTCTAACACAGTTCTCAACCACAGCACTTTTGTCCC
TGGAGATGTTGGCAGTGTCCAGAGGCGTGTTGATGGTCCCCTGAGGGTGGGGGTGCTGCTGGCA
CCAGATGGTAGGGAGATGCCAGGGGTGCTGCTCCACACCCTATGGGACACTGCACAGTACACC
TGGCCTGTGTCCCCACAGCGAGAGCTGGCCCTGGGCAGGCGTGGTCCCTGCGGTGTGTGTTG
GTTGGGATCCTCCACAGTGACAGACGGTGCGCTCTGCCACGTTTCCACACAGCTCTTTTGCT
TGTGGAGCTCACCCCTTTGCAGAGAGCTCATTTCCCTGCGGTCTTTGGCCTGCAGAAGTAAAA
TGAGGGGTGGTGAATTACACCCCTGCTGGTTACACATGGAAACTCAGGAGTGAGAATTTTGT
GGAGAGCAAGAGAGGTGAGACTGGGGTGCTGGCTGCCAGCCAGGCGGTCCCTCAGCCCCCTGGA
GAAGCGGGGTGGGGCCTGCACACCGAGTCCTTCCAGTGAGTCCAGTGATGCTCTCTCCTCTTC
CTCCCAGTCACCTTTCTCTCCAGTGCCACTACTGCGCTTTCGATGCAGAATAATTCAGTATTT
GGCGACTTGAAGTCGGACGAGATGGAGCTGCTCTACTCAGCCTACGGAGATGAGACAGGCGTG
CAGTGTGCGCTGAGCCTGCAGGAGTTTGTGAAGGATGCTGGGAGCTACAGCAAGAAAGTGGTG
GACGACCTCCTGGACCAGATCACAGGCGGAGACCACTCTAGGACGCTCTTCCAGCTGAAGCAG
AGAAGAAATGTTCCCATGAAGCCTCCAGATGAAGCCAAGGTGGGGACACCCTAGGAGACAGC
AGCAGCTCTGTTCTGGAGTTCATGTCGATGAAGTCCTATCCCGACGTTTCTGTGGATATCTCC
ATGCTCAGCTCTCTGGGGAAGGTGAAGAAGGAGCTGGACCCTGACGACAGCCATTTGAACTTG
GATGAGACGACGAAGCTCCTGCAGGACCTGCACGAAGCACAGGCGGAGCGCGGCGGCTCTCGG
CCGTCTCAACCTCAGCTCCCTGTCCAACGCCTCCGAGAGGGACCAGCACCACTGGGAAGC
CCTTCTCGCCTGAGTGTGCGGGGAGCAGCCAGACGTCACCCACGACCCCTATGAGTTTCTTCAG
TCTCCAGAGCCTGCGGCCCTCTGCCAAGACCTAACTCTAGACCACCTTCAGCTCTTTTATTTTA
TTTTTTTAGTTTTTATTTTGCACGTGTAGAGTTTTTGTTCATCAGACAAGGACTTTGATCCTGTC
CCCTTTGGCATGCGGGAAGCAGCCGCGGGGAGGTAATGAATTGTCTGTGGTATCATGTGAGCA
GAGTCTCCAAGCCCCACGAACCTGAGGAGTGGAGTCATACGCGAAGGCCATATGGCCATCGT
GTCAGCAGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGGAGTCATACACGAAG
GGCGTGTGGCCATCGTGTGACGAGAGAGTCTCTGTACACAGCCCCGTGAACCCTGAGGAGTGG
AGTCATACGCGAAGGGTGTGTGGCCAGGCTGCAGAGCTGCGTGCCGTTTGTGTCCGAGCATCA
CGTGTGGCTCCAGCCCTTGTTTCTGCCAGTGTAGACACCTCTGTCTGCCCCACTGTCCTGGGG
TCGCTCTTGGGAGGCACAGGCATGGGTGTGTCTGGCCTCATTTCTGTATCAGTCCAGTGTGTTT
CTGTATAGTTTTGTGTCTCCAGGCAGGCCATGGTAGGGGGCCTCGCAGGGGGCCATTGGGGAGC
ACAGGGCCAGGCTGGGGTGGAGAGAGCTCCCCTGTTTTCTGTTTAATTGATGAGCCTGGGAAA
GGAGTGTGTTCTGCCTGCCCCGTTACAGTGGAGCGTTCGTTGTCCATAAAACGTTTTCTAACTG
GGAA

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FIGURE 550

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119537
><subunit 1 of 1, 104 aa, 1 stop
><MW: 11136, pI: 8.20, NX(S/T): 0
MLAVSRGVL MVPLGLGVLLAPDGREMPGVLLHTLWDTAQYTWPVSP TARAGPGQAWSLRC
VLVGILHSDRR CALPTFP HSSFACGAHPFAESSFPCGLWPAEVK

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 53-59;64-70;97-103

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 74-85

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FIGURE 551

CGCCCTTAGCATGGGTTTCTGCCGCAGCGCCCTGCACCCGCTGTCTCTCCTGGTGCAGGCCATCATGCTGGCCAT
GACCCTGGCCCTGGGTACCTTGCCTGCCTTCCTACCCTGTGAGCTCCAGCCCCACGGCCTGGTGAAGTGCAGTGC
GCTGTTCTGAAGTCTGTGCCCCACTTCTCCATGGCAGCACCCCGTGGCAATGTCACCAGCCTTTCCTTGTCTC
CAACCGCATCCACCACCTCCATGATTCTGACTTTGCCACCTGCCAGCCTGCGGCATCTCAACCTCAAGTGGAA
CTGCCCCGCCGTTGGCCTCAGCCCCATGCACTTCCCCTGCCACATGACCATCGAGCCCAGCACCTTCTTGGCTGT
GCCACCCCTGGAAGAGCTAAACCTGAGCTACAACAACATCATGACTGTGCCTGCGCTGCCCAAATCCCTCATATC
CCTGTCCCTCAGCCATACCAACATCCTGATGCTAGACTCTGCCAGCCTCGCCGGCCTGCATGCCCTGCGCTTCCT
ATTCATGGACGGCAACTGTTATTACAAGAACCCCTGCAGGCAGGCACTGGAGGTGGCCCCGGGTGCCCTCCTTGG
CCTGGGCAGCCTCACCCACCTGTCACTCAAGTACAACAACCTCACTGTGGTGGCCCCGCAACCTGCCTTCCAGCCT
GGAGTATCTGCTGTTGTCTTACAACCGCATCGTCAAACCTGGCGCCTGAGGACCTGGCCAATCTGACCGCCCTGCG
TGTGCTCGATGTGGGCGGAAATTGCCGCCGCTGCGACCACGCTCCCAACCCCTGCATGGAGTGGCCTCGTCACCTT
CCCCAGCTACATCCCGATACCTTCAGCCACCTGAGCCGTCTTGAAGGCCTGGTGTGAAGGACAGTTCTCTCTC
CTGGCTGAATGCCAGTTGGTTCCGTGGGCTGGGAAACCTCCGAGTGCTGGACCTGAGTGAGAAGTTCCTCTACAA
ATGCATCACTAAAACCAAGGCCCTCCAGGGCCTAACACAGCTGCGCAAGCTTAACCTGTCTTCAATTACCAAAA
GAGGGTGTCTTTGCCACCTGTCTCTGGCCCCCTTCCTTCGGGAGCCTGGTGGCCCTGAAGGAGCTGGACATGCA
CGGCATCTTCTTCGCTCACTCGATGAGACCACGCTCCGGCCACTGGCCCGCCTGCCCATGCTCCAGACTCTGCG
TCTGCAGATGAAGTTCATCAACCAGGCCAGCTCGGCATCTTCAGGGCCTTCCCTGGCCTGCGCTACGTGGACCT
GTGCGACAACCGCATCAGCGGAGCTTCGGAGCTGACAGCCACCATGGGGGAGGCAGATGGAGGGGAGAAGGTCTG
GCTGCAGCCTGGGGACCTTGCTCCGGCCCCAGTGGACACTCCCAGCTCTGAAGACTTCAGGCCCAACTGCAGCAC
CCTCAACTTCACCTTGGATCTGTACGGAACAACCTGGTGACCGTGCAGCCGGAGATGTTTGCCAGCTCTCGCA
CCTGCAGTGCCCTGCGCCTGAGCCACAACCTGCATCTCGCAGGCAGTCAATGGCTCCCAGTTCTGCGCCTGACCGG
TCTGCAGGTGCTAGACCTGTCCACAATAAGCTGGACCTCTACCACGAGCACTCATTACGGAGCTACCACGACT
GGAGGCCCTGGACCTCAGCTACAACAGCCAGCCCTTTGGCATGCAGGGCGTGGGCCACAACCTTCAGCTTCGTGGC
TCACCTGCGCACCCCTGCGCCACCTCAGCCTGGCCCCACAACAACATCCACAGCCAAGTGTCCCAGCAGCTCTGCAG
TACGTGCTGCGGGGCCCTGGACTTCAGCGGCAATGCACTGGGCCATATGTGGGCCGAGGGAGACCTCTATCTGCA
CTTCTTCCAAGGCCTGAGCGGTTTGATCTGGCTGGACTTGTCCAGAACCCTGCACACCCTCCTGCCCCAAAC
CCTGCGCAACCTCCCCAAGAGCCTACAGGTGCTGCGTCTCCGTGACAATTACCTGGCCTTCTTTAAGTGGTGGAG
CCTCCACTTCCTGCCCAAACCTGGAAGTCTCGACCTGGCAGGAAACCAGCTGAAGGCCCTGACCAATGGCAGCCT
GCCTGCTGGCACCCGGCTCCGGAGGCTGGATGTGAGCTGCAACAGCATCAGCTTCGTGGCCCCCGGCTTCTTTTC
CAAGGCCAAGGAGCTGCGAGAGCTCAACCTTAGCGCCAACGCCCTCAAGACAGTGGACCACTCCTGGTTTGGGCC
CCTGGCGAGTGGCCTGCAAATACTAGATGTAAGCGCCAACCCCTCTGCACTGCGCCTGTGGGGCGGCCTTTATGGA
CTTCCTGCTGGAGGTGCAGGCTGCCGTGCCCGGTCTGCCAGCCGGGTGAAGTGTGGCAGTCCGGGCCAGCTCCA
GGGCCCTCAGCATCTTTGCACAGGACCTGCGCCTCTGCCTGGATGAGGCCCTCTCCTGGGACTGTTTCGCCCTCTC
GCTGCTGGCTGTGGCTCTGGGCCTGGGTGTGCCCATGCTGCATCACCTCTGTGGCTGGGACCTCTGGTACTGCTT
CCACCTGTGCCTGGCCTGGCTTCCCTGGCGGGGGCGGCAAAGTGGGCGAGATGAGGATGCCCTGCCCTACGATGC
CTTCGTGGTCTTCGACAAAACGCAGAGCGCAGTGGCAGACTGGGTGTACAACGAGCTTCGGGGGCAGCTGGAGGA
GTGCCGTGGGCGCTGGGCACTCCGCCTGTGCCTGGAGGAACGCGACTGGCTGCCTGGCAAACCCCTCTTTGAGAA
CCTGTGGGCCCTCGGTCTATGGCAGCCGCAAGACGCTGTTTGTGCTGGCCCCACACGGACCGGGTCAGTGGTCTCTT
GCGCGCCAGCTTCCTGCTGGCCCAGCAGCGCCTGCTGGAGGACCGCAAGGACGTCTGGTGGTGGTGGTGGTGGTGG
CCCTGACGGCCGCGCTCCCGCTACGTGCGGCTGCGCCAGCGCCTCTGCCGCCAGAGTGTCTCCTCTGGCCCCA
CCAGCCCAGTGGTCAGCGCAGCTTCTGGGCCAGCTGGGCATGGCCCTGACCAGGGACAACCAACCACTTCTATAA
CCGGAACCTCTGCCAGGGACCCACGGCCGAATAGCCGTGAGCCGGAATCCTGCACGGTGCCACCTC

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FIGURE 552

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119714
><subunit 1 of 1, 1032 aa, 1 stop
><MW: 115799, pI: 8.61, NX(S/T): 12
MGFCRSALHPLSLLVQAIMLAMTLALGTLPAFLPCELQPHGLVNCNWFLKSVPHFSMAA
PRGNVTSLSLSSNRIHHLHDSDFAHLPRLNLKWNCPVGLSPMHFPCHMTIEPSTFL
AVPTLEELNLSYNNIMTVPALPKSLISLSLSTNIMLDSASLAGLHALRFLFMDGNCY
KNPCRQALEVAPGALLGLGSLTHLSLKYNNTLVVPRNLPSSEYLLLSYNRIVKLAPEDL
ANLTALRVLDVGGNCRCDHAPNPCMECPRHFPQLHPDTFSHLSRLEGLVLKDSLSLWLN
ASWFRGLGNLRVLDLSENFYKCIKTKALQGLTQLRKLNLNLSFNYQKRVSEFAHLSLAPSF
GSLVALKELDMHGIFFRSLDETTLRPLARLPMLQTLRLQMNFINQAQLGIFRAFPGLRYV
DLSDNRISGASELTATMGEADGGKVLQPGDLAPAPVDTPSSEDFRPNCSTLNFTLDLS
RNNLVTVPQEMFAQLSHLQCLRLSHNCISQAVNGSQFLPLTGLQVLDLSHNKLDLYHEHS
FTELPRLEALDLSYNSQPFQGMQGVGHNFSEFAHLRTRLRHLSLAHNNIHSQVSQQLCSTSL
RALDFSGNALGHMWAEGDLYLHFFQGLSGLIWLDSLQNRHLHTLLPQTLRNLPKSLQVRL
RDNYLAFFKWWSLHFLPKLEVLDLAGNQLKALTNGSLPAGTRLRRLDVSCNSISFVAPGF
FSKAKELRELNLSANALKTVDHSWFGPLASALQILDVSANPLHCACGAAFMDFLLEVQAA
VPGLPSRVKCGSPGQLQGLSIFAQDLRLCLDEALSWDCLFALLAVALGLGVPMHLHLCG
WDLWYCFHLCLAWLPWRGRQSGRDEDALPYDAFVVFDTQSAVADWVYNEIRGQLEECRG
RWALRLCLEERDWLPKTLFENLWASVYGSRKTLFVLAHTDRVSGLLRASFLLAQQRLLE
DRKDVVVLVILSPDGRRSRYVRLRQRLCRQSVLLWPHQPSGQRSFWAQLGMALTRDNHFF
YNRNFCQGPTAE

Important features of the protein:**Signal peptide:**

Amino acids 1-30

Transmembrane domain:

Amino acids 818-835

N-glycosylation sites:Amino acids 64-68;129-133;210-214;242-246;300-304;340-344;
469-473;474-477;513-517;567-571;694-698;731-735**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

Amino acids 347-351

Tyrosine kinase phosphorylation site:

Amino acids 863-871

N-myristoylation sites:Amino acids 27-33;41-47;63-69;193-199;361-367;409-415;
563-569;607-613;695-701;794-800;929-935;945-951;
1010-1016**Amidation site:**

Amino Acids 974-978

Leucine zipper patterns:

Amino acids 204-226;644-666;814-836

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FIGURE 553

GGCGTGGGACGTGCTGCGGCGTCCTAGCTGGCTTACAGGGCGGCGGGGGTGTGTGTCCTCT
GTTAAGAGTGCTACTCGCCCCGGGGTTGATCTGTGCATGCCACTCCTGGGTGAGACGGTGAGGT
CGGCGTCTGCGAGGACGCGGCGGTGGAGTAGAAGGGCAGCCGGAGACAGGCCCGGCGCCCCCTT
CCGAGGCTAGACGGCCCCAGCTTCGCGGGGATCATGGCATTGCTGGTGGACCGAGTGCGGGGC
CACTGGCGAATCGCCGCCGGGCTCCTGTTCAACCTGCTGGTGTCCATCTGCATTGTGTTCCCTC
AACAAATGGATTTATGTGTACCACGGCTTCCCCAACATGAGCCTGACCCTGGTGCACCTTCGTG
GTCACCTGGCTGGGCTTGTATATCTGCCAGAAGCTGGACATCTTTGCCCCCAAAGTCTGCCG
CCCTCCAGGCTCCTCCTCCTGGCCCTCAGCTTCTGTGGCTTTGTGGTCTTCACTAACCTTTCT
CTGCAGAACAAACACCATAGGCACCTATCAGCTGGCCAAGGCCATGACCACGCCGGTGATCATA
GCCATCCAGACCTTCTGCTACCAGAAAACCTTCTCCACCAGAATCCAGCTCACGCTGATTCCT
ATAACTTTAGGTGTAATCCTAAATTCTTATTACGATGTGAAGTTTAATTTCTTGGAATGGTG
TTTGCTGCTCTTGGTGTTTTAGTTACATCCCTTTATCAAGTGTGGGTAGGAGCCAAACAGCAT
GAATTACAAGTGAACCTCAATGCAGCTGCTGTACTACCAGGCTCCGATGTCATCTGCCATGTTG
CTGGTTGCTGTGCCCTTCTTTGAGCCAGTGTTTGGAGAAGGAGGAATATTTGGTCCCTGGTCA
GTTTCTGCTTTGCTTATGGTGCTGCTATCTGGAGTAATAGCTTTCATGGTGAACCTTATCAATT
TATTGGATCATTGGGAACACTTCACCTGTCACCTATAACATGTTCCGGACACTTCAAGTTCTGC
ATTACTTTATTTCGGAGGATATGTTTTATTTAAGGATCCACTGTCCATTAATCAGGCCCTTGGC
ATTTTATGTACATTATTTGGCATTCTCGCCTATACCCACTTTAAGCTCAGTGAACAGGAAGGA
AGTAGGAGTAAACTGGCACAACGTCCTTAATTGGGTTTTTGTGGAGAAAAGAATGTTGTCCCA
AGAAGATAAAAAATATTGTTAAGTGTGCAAGTTATTA

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FIGURE 554

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA125170
><subunit 1 of 1, 313 aa, 1 stop
><MW: 35066, pI: 9.39, NX(S/T): 5
MALLVDRVRGHWRIAAGLLFNLLVSICIVFLNKWIYVYHGFPNMSLTLVHFVVTWLGLYI
CQKLDIFAPKSLPPSRLLLLALSFCGFVVFTNLSLQNTIGTYQLAKAMTTPVIIAIQTF
CYQKTFSTRIQLTLIPITLGVIILNSYYDVKFNFGLGMVFAALGVLVTSLYQVWVGAKQHEL
QVNSMQLLYYQAPMSSAMLLVAVPFFEPVFEGGGIFGPWSVSALLMVLLSGVIAFMVNLS
IYWIIGNTSPVTYNMFGHFKFCITLFGGYVLEKDP L SINQALGILCTLFGILAYTHFKLS
EQEGSRSKLAQRP

Important features of the protein:**Signal peptide:**

Amino acids 1-27

Transmembrane domains:

Amino acids 46-60;75-90;153-167;192-208;221-237

N-glycosylation sites:

Amino acids 43-47;92-96;97-101;238-242

N-myristoylation sites:

Amino acids 17-23;57-63;140-146;155-161;162-168;283-289

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FIGURE 555

GTTAGGCAGAGCCAAGGTGGTTGCAGACCTGGAATCAGAACAGCTTTTAGACCAACCTGAAAG
CAGGAATGTAAGCACTGTTACAGAGATTTTCGTCTTTGGCTTATTGTGCCTGCAGAGTCTAG
TGCTTCTTTGCCAGCTGTGCTGACTCAGCACTCCATGCCTGTTTTCTGGAACCAGTCCCTGGA
GCTGGGCCATGTTTTGATTGACAGTGTGGAGCTAGCCCAGCAAGTACTCTACATGCAACCCCC
CACCCAGGCACTACCTCTGCTCCTCCTCCATGGCCTCCTGCTACACCGGCAGCTCTATGGAAC
AAGGCTGCAGGCACACAGGGGGCGCTGGAGTCAAGTGACTCTAACCCAGGTTCTTCAGACCCA
AGACCAGCTGTGGGCAAGTCTTAGCAATCCCCGTGCTGCCATGCAAGAGCTGGCTGCTTCAGT
TTTCTACGGGGGTCTCTGGGGGACACTGAGGACAGGGAGGCCCTGATTAGCCTCACACAAGC
CTGCCTGAGCCCCAGTAGTGGGAGCTGGGTCCAGCCACACACACCTCAGTCTTTGCTGGCCAC
GCTCATGCCCCCTCCCAGCTAAGGGAGCTGGATGCAATGGCAGAGTGCAAGGCCCAGATGCACC
TACTGCCCTCACCACTTGAACCCCCGGCTCTGCGGACTGAGTGAGGGCCCCCAAGCCTGGCTGT
TGCGACGCCAGAGTCGCGCTCTCTTGAGTGCGCTGCAGCGGAGTTCACCCGTGTGGGTTCTTG
AGTCTCGAAGAGGCGCCAGCTTGCGGAAAGGCGACTGCGGCAACGCCTAGTGCAAGTCAACCG
GAGGCTGGAGTCACTGCAGGATCTGCTGACCCACGTGATTCGCCAAGACGAGTCCGACGCCCC
GTGGTCAGTGCTGGGGCCAAATGCACGGCGGCCTCTGGAGGGCGTCTTAGAGACCGAGGCTCT
AGAACTGAGCCAGTTGGTGGGCACGCTACAACGCGACCTTGATTGCCTGTTGCAGCAGCTGAA
GGGCGCACCCCCGTGCCCCCTCCCGCCGCTGTGCTGCGGTGGCCACGCTCTCTGGACTGGCCG
CCTACCCTTGCCCTGGCGACCTCATGCGCCGGCCGGTCCGCAGCCGCCCTGGCACTGGCTGCG
ACAGTTGTCGCGCCCGTGGGCAACTGTTGGTTCTGTTACTTGGGCGTGGGCGCGGACGCGAGCAG
TGATGTACCAGAGCGCGTCTTCCACCTGTCAGCCTTTCGCCACCCGCGCCGCTGCTGCTGGC
ATTGCGTGGGGAAGCTGCCCTGGACCAGAATGTGCCCAGCTCGAATTTCCCTGGTAGCCGAGG
CTCGGTCTCCAGTCAGCTCCAGTATAAACGTCTGGAGATGAACAGCAACCCTCTGCACTTCAG
GGTGGAGAATGGTCCAAATCCCACGGTTCCAGAGAGAGGGCTGCTGCTGATCGGGCTACAGGT
CCTACATGCGGAGTGGGACCCAATAGCTGGAGCCTTGCAAGACAGTCCTTCCAGCCAACCCAG
CCCTCTGCCTCCCGTCAGCATCAGCACACAGGCCCCCGGGCACCAGTGACCTGCCAGCCCCAGC
CGACCTGACTGTGTACTCGTGTCTGTGTACATGGGAGGGCCCCTTGGCACCGCTAAGCTGCA
GAGCAGGAACATCGTGATGCATCTGCCTTTACCCACCAAGCTCACCCCCAACACCTGTGTCCA
AAGGAGGGTCCATGTGTGCAGCCCACCCCTGTCTTGAGCCCGTCTACCAAATAAAGTTGTAG
TGATTCCA

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FIGURE 556

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129594
><subunit 1 of 1, 162 aa, 1 stop
><MW: 17598, pI: 6.58, NX(S/T): 1
MPVFWNQSLELGHVLIIDSVELAQQVLYMQPPTQALPLLLHGLLLHRQLYGTRLQAHRGR
WSQVTLTQVLQTQDQLWASLSNPRAAMQELAASVFYGGPLGDTEDREALISLTQACLSPS
SGSWVQPHTPQSLLATLMPLPAKGAGCNGRVQGPDAPTALT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-45

N-glycosylation site:

Amino acids 6-10

N-myristoylation sites:

Amino acids 97-103;144-150

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FIGURE 557

GACCTTGAGCCCTCGAAAGCGACATGGCGGTTCTCTTAAAGCTGGGCGTTCTCTGCAGTGGCC
AAGGAGCTCGAGCTCTCCTACTCCGAAGCCGGGTGGTCAGACCCGCTTATGTGTCAGCATTTT
TCCAGGACCAGCCTACCCAAGGACGGTGTGGTACCCAGCACATTCACCTGTCACCAAGCCACC
ACTCTGGTTCCAAGGCTGCATCTCTCCACTGGACCAGTGAGAGGGTTGTCAGTGTTCTGCTCT
TGGGGCTGATCCCTGCTGGGTACTTGAATCCCTGCTCTGTGGTGGACTACTCTCTGGCTGCAG
CCCTCACCCCTGCACAGTCACTGGGGCCTTGGACAAGTGGTTACCGACTACGTTTCATGGGGACA
CCCTGCCGAAGGCTGCCAGGGCAGGCCTCTTGGCACTCTCAGCTTTGACCTTTGCTGGGCTTTGC
TACTTCAATTACCACGATGTCGGCATCTGCAGAGCGGTTGCCATGCTGTGGAAGCTCTTGACCT
GGGTGCAGCACTTTGATTGTGTGCCTCCTTGCCTCTGCTTTACCAATGCCGTTACCTCGCAG
TGAGGGGGGATGAAGGATAAGCCCATTTGGTGGGCAGAATGTCTTCTAATTACATGGTTATTTT
CAGAATTTATTTGTTGAGGAAGAGGTTTGAGGAGTTAGGTTCGACCATTCGTGAGTCTGTGTT
CCATACTCCACTGAGTGTGGGCACTAGCTCACAGCCTCGCGGTGAGACTGAACATTTTCATGAG
CTCATGTTGCCTTTGACCACCATTTCTTAAGGAGAGCCAGCTGATTGCTGTCAGGATAAGAGC
ATCTCTTCAGCCAGGAGGGAGGCCTGTTCCCTCCTGAGTTAGACTTTGCATGAAGCTCGAAAG
TATTCCCTTTGGAACCTCCCATTCTTGTTTCAGGTGACACCAGCTCTGTTGATGGCTCTGCTTC
TAGGGAACATTTAATCAGGAGATGCTCTCAATGACTAATTTGTCTAAGTCTTAGGAAGGAGGT
TGAGGAAAGCTGGATTTAGACAAGTTCAATTTAGGGAGTTCTCCTTGTTTGTGGATTAAAATA
TGACAGATTGCAAACAGACTACTCTTCAAATGTATCTCAATTGTGCAGAAGTGAGCTGTCCAA
AAGTATAAGACTAAGTGATAAACTGTCTTCCCACCGTGGGAGTTGTTAATGAGAAAGAAAGTG
TACTCTGAAAAAACAAGGGGG

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FIGURE 558

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA129793
><subunit 1 of 1, 159 aa, 1 stop
><MW: 17014, pI: 9.38, NX(S/T): 0
MAVLLKLGVLCSGQGARALLRSRVVRPAYVSAFLQDQPTQGRCGTQHIHLSPSHHSGSK
AASLHWTSEVVSVLLLGLIPAGYLNPCSVVDYSLAAALTLHSHWGLGQVVTDYVHGDTL
PKAARAGLLALSALTFAGLCYFNYHVDVGICRAVAMLWKL

Important features of the protein:**Signal peptide:**

Amino acids 1-15

Transmembrane domains:

Amino acids 71-88;126-140

Glycosaminoglycan attachment site:

Amino acids 12-16

N-myristoylation sites

Amino acids 8-14;58-64;78-84;108-114;148-154

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FIGURE 559

CCCAGCCCCGCGTTTCGGCTGCTCTCGAGGAGGCCGGAGTCCCCGGAGACGATGCGCCCCGCGC
AGCCGCCTGCGCCTGCGGGAGCCGGCTGCCCTTGAGATGGAGTTGCTGCCTCTTTGGCTCTGC
CTGGGTTTTCACTTCCTGACCGTGGGCTGGAGGAACAGAAGCGGAACAGCCACAGCAGCCTCC
CAAGGAGTCTGCAAGTTGGTGGGTGGAGCCGCTGACTGCCGAGGGCAGAGCCTCGCTTCGGTG
CCCAGCAGCCTCCCGCCCCACGCCCCGGATGCTCACCTGGATGCCAACCTCTCAAGACCCTG
TGGAATCACTCCCTCCAGCCTTACCCTCTCCTGGAGAGCCTCAGCCTGCACAGCTGCCACCTG
GAGCGCATCAGCCGCGGCGCCTTCCAGGAGCAAGGTCACCTGCGCAGCCTGGTCCTGGGGGAC
AACTGCCTCTCAGAGAACTACGAAGAGACGGCAGCCGCCCTCCACGCCCTGCCGGGCTGCGG
AGGCTGGACTTGTGAGGAAACGCCCTGACGGAGGACATGGCAGCGCTCATGCTCCAGAACCTC
TCCTCGCTGCGGTCCGTGTCCCTGGCGGGGAACACCATCATGCGGCTGGACGACTCCGTCTTC
GAGGGCCTGGAGCGTCTCCGGGAGCTGGATCTGCAGAGGAACTACATCTTCGAGATCGAGGGC
GGCGCTTTTCGACGGCCTGGCTGAGCTGAGGCACCTCAACCTGGCCTTCAACAACCTCCCCTGC
ATCGTGGACTTCGGGCTCACGCGGCTGCGGGTCTCAACGTGAGCTACAACGTCTGGAGTGG
TTCCTCGCGACCGGGGGAGAGGCTGCCTTCGAGCTGGAGACGCTGGACCTGTCTCACAACCAG
CTGCTGTTCTTCCCGCTGCTGCCCCAGTACAGCAAGTTGCGGACCCTCCTGCTGCGCGACAAC
AACATGGGCTTCTACCGGGACCTGTACAACACCTCGTCGCCGAGGGAGATGGTGGCCCAGTTC
CTCCTCGTGGACGGCAACGTGACCAACATCACCAACGTCAGCCTCTGGGAAGAATTCTCCTCC
AGCGACCTCGCAGATCTCCGCTTCCTGGACATGAGCCAGAACCAGTTCCAGTACCTGCCAGAC
GGCTTCCTGAGGAAAATGCCTTCCCTCTCCACCTGAACCTCCACCAGAATTGCCTGATGACG
CTTCACATTTCGGGAGCACGAGCCCCCGGAGCGCTCACCGAGCTGGACCTGAGCCACAACCAG
CTGTGCGGAGCTGCACCTGGCTCCGGGGCTGGCCAGCTGCCTGGGCAGCCTGCGCTTGTTCAAC
CTGAGCTCCAACCAGCTCCTGGGCGTCCCCCTGGCCTCTTCGCCAATGCTAGGAACATCACTAC
ACTTGACATGAGCCACAATCAGATCTCACTTTGTCCCCTGCCAGCTGCCTCGGACCGGGTGGG
CCCCCTAGCTGTGTGGATTTTCAGGAATATGGCATCTTTAAGGAGCCTGTCTCTGGAGGGCTG
TGGCCTGGGGGCATTGCCAGACTGCCCATTTCCAAGGGACCTCCCTGACCTACTTAGACCTCTC
AAGCAACTGGGGGGTTCTGAATGGGAGCCTCGCCCCACTCCAGGATGTTGCCCCCATGTTACA
GGTCCTGTCTCTCAGGAACATGGGCCTCCACTCCAGCTTTATGGCGTTGGACTTCTCTGGGTT
TGGGAATCTCAGGGACTTAGATCTGTGCGGGAATTGCTTGACCACCTTCCAAGGTTTGGGGG
CAGCCTGGCCCTGGAGACCCTGGATCTCCGTAGAACTCGCTCACAGCCCTTCCCCAGAAGGC
TGTGTCTGAGCAGCTCTCGAGAGGTCTGCGGACCATCTACCTCAGTCAGAATCCATATGACTG
CTGTGGGGTGGATGGCTGGGGGGCCCTGCAGCATGGGCAGACGGTGGCCGACTGGGCCATGGT
CACCTGCAACCTCTCCTCCAAGATCATCCGCGTGACGGAGCTGCCCGGAGGTGTGCCTCGGGA
CTGCAAGTGGGAGCGGCTGGACCTGGGCCTGCTCTACCTCGTGCTCATCCTCCCCAGCTGCCT
CACCTGCTGGTGGCCTGCACTGTCATCGTCCTCACTTTTAAGAAGCCTCTGCTTCAGGTCAT
CAAGAGCCGCTGCCACTGGTCCTCCGTTTACTGACCTGGCTGTGTGCCAAGACTCGAAATTCG
GTCCGCACACAACAGGACACTTTCTCTGCCAGCTTTCAAGATGTGATGCAGAGGCCAAGTCTG
ACGAATTGAAGTTTCAATTAAAATTTAATATGTTTCCATTCTCATCGCCACCCCAACCCCG
CCCCACCACCGCCCAAGTTCTTTTCCATCATTATAATTATCCTTATTATCTTGGTAAAAT
ATTTATTAAGTGACTTTTTTCAGAAATAAAAGGCAACGTGTCTCATAAATATTTTTTAAAAAA
AAAAAAAAAAAAAA

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FIGURE 560

><subunit 1 of 1, 692 aa, 1 stop
><MW: 76366, pI: 6.07, NX(S/T): 11
MELLPLWLCLGFHFLTVGWRNRS GTATAASQGVCKLVGGAADCRGQSLASVPSSLPPHAR
MLTLDANPLKTLWNHSLQPYPLLESLSLH SCHLERISRGA FQEQGHLRSLVLGDNCLSEN
YEETAALHALPGLRRLDLSGNALTEDMAALMLQNLSSLRSVSLAGNTIMRLDDSVFEG
ERLRELDLQ RNYIFEIEGGAFDGLAELRHLNLA FNNLPCIVDFGLTRLRLVNLVSYNVLEW
FLATGGEEAAFELETLDLSHNQLLFFPLLPOYSKLR TLLLRDNNMGFYRDLYNTSSPREMV
AQFLLVDGNVTNITT VSLWEEFSSSDLADLRFLDMSQNQFQYLPDGFLRKMPSLSHLNLH
QNCLMTLHIREHEPPGALTELDLSHNQLSELHLAPGLASCLGSLR LFNLSNQLLGVP
PG LFANARNITTLDMSHNQISLCPLPAASDRVGPPSCVDFRNMASLRSLSLEGCGLGALPDC
PFQGTSLTYLDLSSNWGV LNGSLAPLQDVAPMLQVLSLRNMGLHSSFMALDFSGFGNLRD
LDLSGNCLTTFPRFGGSLALETLDLRRNSLTALPQKAVSEQLSRGLRTIYLSQNPYDCCG
VDGWGALQHGQTVADWAMVTCNLSSKIIRVTELPGGVPRDCKWERLDLGLLYLV LILPSC
LTLLVACTVIVLTFKKPLLQVIKSRCHWSSVY

Important features of the protein:**Signal peptide:**

Amino acids 1-18

Transmembrane domain:

Amino acids 651-672

N-glycosylation sites:Amino acids 21-25;74-78;155-159;232-236;292-296;309-313;
312-316;408-414;427-431;500-504;622-626**Glycosaminoglycan attachment site:**

Amino acids 533-537

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 566-570

N-myristoylation sites:Amino acids 24-30;39-45;45-51;141-147;199-205;245-251;
308-314;396-402;416-422;420-426;471-477;
484-490;497-503;522-528;545-551;555-561;610-616**Prokaryotic membrane lipoprotein lipid attachment site:**

Amino acids 657-668

Leucine zipper patterns:

Amino acids 48-70;492-514

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FIGURE 561

TGGCCTACTGGAAAAAAAAAAAAAAAAAAAAAAAAAGTCACCCGGGCCCCGCGGTGGCCACAACAT
GGCTGCGGCGCCGGGGCTGCTCTTCTGGCTGTTTCGTGCTGGGGGCGCTCTGGTGGGTCCCGGG
CCAGTCGGATCTCAGCCACGGACGGCGTTTCTCGGACCTCAAAGTGTCGGGGACGAAGAGTG
CAGCATGTTAATGTACCGTGGGAAGCTCTTGAAGACTTCACGGGCCCTGATTGTCGTTTTGT
GAATTTTAAAAAAGGTGACGATGTATATGTCTACTACAACTGGCAGGGGGATCCCTTGAAC
TTGGGCTGGAAGTGTTGAACACAGTTTTTGGATATTTTCCAAAAGATTTGATCAAGGTACTTCA
TAAATACACGGAAGAAGAGCTACATATTCCAGCAGATGAGACAGACTTTGTCTGCTTTGAAGG
AGGAAGAGATGATTTTAATAGTTATAATGTAGAAGAGCTTTTAGGATCTTTGGAAGTGGAGGA
CTCTGTACCTGAAGAGTCGAAGAAAGCTGAAGAAGTTTCTCAGCACAGAGAGAAATCTCCTGA
GGAGTCTCGGGGGCGTGAACCTTGACCTGTGCCTGAGCCCGAGGCATTCAGAGCTGATTCAGA
GGATGGAGAAGGTGCTTTCTCAGAGAGCACCGAGGGGCTGCAGGGACAGCCCTCAGCTCAGGA
GAGCCACCCTCACACCAGCGGTCCTGCGGCTAACGCTCAGGGAGTGCAGTCTTCGTTGGACAC
TTTTGAAGAAATTCTGCACGATAAATTGAAAGTGCCGGGAAGCGAAAGCAGAACTGGCAATAG
TTCTCCTGCCTCGGTGGAGCGGGAGAAGACAGATGCTTACAAAGTCCTGAAAACAGAAATGAG
TCAGAGAGGAAGTGGACAGTGC GTTATTCATTACAGCAAAGGATTTTCGTTGGCATCAAAATCT
AAGTTTGTTTTTACAAAGATTGTTTTTAGTACTAAGCTGCCTTGGCAGTTTGCATTTTTTGAGCC
AAACAAAATATATTATTTTCCCTTCTAAGTAAAAAAAAAAAAAAAAAAAAA

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FIGURE 562

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131639
><subunit 1 of 1, 303 aa, 1 stop
><MW: 33900, pI: 4.81, NX(S/T): 2
MAAAPGLLFWLFLGALWWVPGQSDLSHGRRFSDLKVCGDEEC SMLMYRGKALEDFTGPD
CRFVNFKKGDDVYVYYKLAGGSLELWAGSVEHSFGYFPKDLIKVLHKYTEEELHIPADET
DFVCFEGGRDDFNSYNVEELLGSLELEDSVPEESKKAEEVSQHREKSPEESRGRELD PVP
EPEAFRADSEEDGEAFSESTEGLOQGQPSAQESH PHTSGPAANAQGVQSSLDTFEEILHDK
LKVPGSESRTGNSSPASVEREKTDAYKVLKTEMSQ RSGQCVIHYSKGFRRWHQNL SLFYK
DCF

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation site:

Amino acids 294-298

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 67-76

N-myristoylation sites:

Amino acids 205-211;225-231;277-283

Amidation site:

Amino acids 28-32

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FIGURE 563

GCCAGCCGTGGGATTAGGCTTCGCCGGCTACGATTGCGGCCCCCATCTTCTGACTTTTCCTCG
TGTGACCCATCTTTTCAAATTCCTTACCTGAGGAAGGAGCCCGATTACAAGGATATTTACCT
GCTCCTACCCTGATCTAGGGACGAGGATGGGAAGACCGCCTGTGGCCATGAGCCCTCCCCGGT
GCTCCTGGGGCTAAGGCTGGGGCTGCAGCCATGGGGGCTGGGTGAGCCCCAGGCCTGGTTGCTG
GGTCTGCCCACAGCTGTGGTCTATGGCTCCCTGGCTCTCTTCACCACCATCCTGCACAATGTC
TTCCTGCTCTACTATGTGGACACCTTTGTCTCAGTGTACAAGATCAACAAAATGGCCTTCTGG
GTCGGAGAGACAGTGTTTCTCCTCTGGAACAGCCTCAATGACCCTCTCTTCGGTTGGCTCAGT
GACCGGCAGTTCCTCAGCTCCCAGCCCCGCCTGTGTGGAGAGGAGCTGCTTGTGGGCAGTGAG
GAGGCGGACAGCATCACCTTGGGCCGGTATCTCCGGCAGCTGGCACGCCATCGGAACTTCCTG
TGGTTCGTGAGCATGGACCTGGTGCAGGTGCAGTGGCTCACGCCTGTAATCCCAGCACTTCGG
GACGCCAAGGTGGAAAGACCGCTTGAGCCCAGGAGTTCGAGGCTGCAATTGAGTTATGATTGCA
CCACTGCACTCCAGCCTGGGCGGCAGAGAAAGGCTCCATCTCTAAAAAAGAAGAGCTAAGTG
CTGTACCTAAACATGCAGTATATAAACTGGCTGAACTTAGAAATAAACTGTTTTCATGTTAT
GAAAA

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FIGURE 564

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131649
><subunit 1 of 1, 153 aa, 1 stop
><MW: 17603, pI: 7.42, NX(S/T): 0
MGLGQPQAWLLGLPTAVVYGSLALFTTILHNVFLLYYVDTFVSVYKINKMAFWVGETVFL
LWNSLNDPLFGWLSDRQFLSSQPRLCGEELLVGSEEADSI TLGRYLRQLARHRNFLWFVS
MDLVQVQWLTPVIPALRDAKVERPLEPRSSRLQ

Important features of the protein:**Signal peptide:**

Amino acids 1-20

N-myristoylation sites:

Amino acids 4-10;12-18;93-99

Leucine zipper pattern:

Amino acids 102-124

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FIGURE 565

CGGCACGAGTAAAATGGAGATAATATCACCAATGCACTCAGCCCTAGCCACTGCATTGCTGTTA
CTGATAACCATTACTGCTGCTACGTCGTTTTTTTGATGGCTCAGCCCTTAGGGAAGGGGGATCA
AGGGAGAAGCCCGGACCTTCCCGCAGGAGGTGGGCTGGGCACAGCCCTGAACCATGGAGGTCA
CCCACCCTGAGGTCGGGACCTGGGTTCCTTCCTATCCACTGGGGGTCCCAGCCTTTGTCTTC
ATCTCTCCAGGTCCCAGCCCTTCACAGTGGGCACTTCCCTGCCTGTGACGGAGGCCCCAGCCA
TCTCC

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FIGURE 566

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131652
><subunit 1 of 1, 89 aa, 1 stop
><MW: 9688, pI: 11.49, NX(S/T): 0
MHSALATALLLLIIPLLLLRRFFDGSALREGGSREKPGPSRRRWAGHSPEPWRSPTLRSGP
GFPSYPLGVPAFVFISPGSPSQWALPCL

Important features of the protein:

Signal peptide:

Amino acids 1-18

Glycosaminoglycan attachment site:

Amino acids 58-62

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FIGURE 567

AGTCTAGCAGGAAAGGAGAGGGAGCTTTCCCCGAAGACCCTCCTGGACCAGCCCCAGGCTCCT
GTGCTGGTTGCACGCCAGGGCCTGTACTGACCACCTCCACGTGCCACTGGGGCTGTAAGGAGGA
ATGGCGGCCGTGGGCAGCCTGCTTGGCCTGGCAGCCTCTTCCTGGCTAGGGGGCCAGAACGCC
TCTGACCACAGCCTGTGGCTCCTGAGGAAGCCCCGAGGCTCATCCTGCCCCGGCACGGGTCAC
CAGCTCTGCCGGCTGAGGCAGAGCACCGTGAAGGCCACCGGACCTGCACTCCGCCGCCTGCAC
ACATCCTCCTGGCGAGCTGACAGCAGCAGGGCCTCACTCACTCGTGTGCACCGCCAGGCTTAT
GCACGACTCTACCCCGTGCTGCTGGTGAAGCAGGATGGCTCCACCATCCACATCCGCTACAGG
GAGCCACGGCGCATGCTGGCGATGCCCATAGATCTGGACACCCTGTCTCCTGAGGAGCGCCGG
GCCAGGCTGCGGAAGCGTGAGGCTCAGCTCCAGTCGAGGAAGGAGTACGAGCAGGAGCTCAGT
GATGACTTGCATGTGGAGCGCTACCGACAGTTCTGGACCAGGACCAAGAAG**TGA**CCGTGGCTC
CAGCCACCCCGGGACATTGCTAAGATGGGAGGGCTGTTCTTAAATCACTCGTTCTTGAAGCTGC

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FIGURE 568

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA131658
><subunit 1 of 1, 164 aa, 1 stop
><MW: 18903, pI: 11.08, NX(S/T): 1
MAAVGSLLGLAASSWLGGQNASDHSLWLLRKPRGSSCPGTGHQLCRLRQSTVKATGPALR
RLHTSSWRADSSRASLTRVHRQAYARLYPVLLVKQDGSTIHIRYREPRRMLAMPIDLDLTL
SPEERRARLRKREAQLQSRKEYEQELSDDLHVERYRQFWTRTKK

Important features of the protein:**Signal peptide:**

Amino acids 1-18

N-glycosylation site:

Amino acids 20-24

N-myristoylation sites:

Amino acids 5-11;9-15;17-23;18-24

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FIGURE 569

GGTGCCAAGGGTTTCGGGGGGGAGCACTGAGGCTTTAGCAGCTCTCCTGTATCCTCATTTGCAT
CCTCCTGTAGCAGCTGGAAAATTCAGATTACAGGTGAAATTCCCTGGCTGGCAATCTTCTGTA
TATGGACACAGTGATGTGCCAGAAGGGCTTTGCATCCCTGAGACTGAAGGAAGCTCCATTTTT
GGAGCCCTCCCACACCTTGCTCTGTGTGCCTCTCATTTCTGATTTGAATTCTTATTTTGCTATA
TGATGAAGCTGTAATCCTAAGTTTAAAAAGGGGAGTAGGTATTGACATCATGGTAGAAATAGG
CTGTCTTATGGAAGTGTAGTTAGGGATCACAGCCTATTGGACCAGCCCCAGCCTTAGCAGCAG
TTCTGTACACTGATTCTTCCAGATTAGTCTACGTTCCCTCGAACAGACCTATGCCATGGGTTA
CAACTACAATTTGTTGTGCGATTAGAGTTAACTTACAGACTCTCAAAACCCCATTTCTTTGGGTT
TAGGCAACTTCCAGAAGTAGTCATTTATTTGAATTTTAGTCTAAGATCAACTGAATTAGGGAG
GTTTGAAAGTGTAAGCAAATCGTACATTCCCAAACACTTTGTAAAGAAGGAATGGGTAGTG
TCAACTAAAGGAATGGTGTGCATCCAGCAAAGAGAGACCGAAAGCAAAGTCATAAACC
ATGCCCCACGAGCTCAGCTGTCCTGCTCCGTGTCCTCTCCATACCCTTGTTGACTGTGCTCATA
TTAGCCAGAGACCTAAGTGCTCTTGGAGGATGTCCCTGGGGCCCCCTCCCCCTCCGCTGTCAC
TGTCTACTTCCTGATCCTCTCTTCTGTGCGAGGAGAGGTCCAGGCCTTCTATGAGGACCTGAGT
GGCCGGCAGTACGTGAATGAAGTCTTCAACTTCAGCGTGGACAAGCTCTATGACCTCCTCTTC
ACCAACTCGCCCTTCCAGCGGGATTTTCATGGAGCAGCGGCGCTTCTCTGATATCATCTTCCAT
CCATGGAAAAAGGAGGAGAATGGAAACCAGAGCCGAGTGATTCTTTACACCATCACCTTACC
AACCCTCTGGCTCCCAAACACTGCCACTGTCAGGGAGACACAGACCATGTACAAGGCGAGCCAG
GAGAGTGAATGTTACGTGATAGATGCCGAAGTCCTCACCCACGACGTGCCCTACCACGACTAC
TTCTACACAATCAATCGCTACACGCTCACCCGTGTGGCTCGGAACAAGAGCCGACTCAGGGTC
TCCACAGAGCTGCGCTATCGAAAACAGCCCTGGGGGTTAGTGAAAACGTTTCATCGAGAAGAAC
TTCTGGAGTGGGCTGGAGGACTACTTCCGCCATTTAGAGAGCGAGCTGGCCAAAACGGAGAGC
ACTTATTTGGCTGAGATGCACAGACAATCTCCCAAAGAGAAGGCCAGCAAGACTACAACGGTG
CGGAGGAGGAAGCGTCCCCATGCCACCTGCGAGTCCCTCACCTGGAAGAGGTGATGAGCCCG
GTCACCACGCCCACAGATGAGGATGTGGGCCACAGGATCAAACATGTGGCAGGTTCCACACAG
ACGCGGCATATCCCGGAGGACACCCCCAACGGTTTCCACCTGCAGAGCGTGTCCAAGCTGCTG
CTGGTTATCAGCTGTGTTCTGGTGCTGCTGGTCATCCTTAACATGATGCTCTTCTACAAACTC
TGGATGTTGGAATACACCACGCAGACCCTCACTGCCTGGCAGGGTCTAAGGCTCCAAGAAAGG
TTACCCCAGTCTCAGACAGAATGGGCCCAGCTCTTAGAGTCCCAACAAAAGTACCACGATACT
GAGCTCCAAAATGGAGGGAAATCATCAAATCCTCAGTGATGCTCCTTGACCAGATGAAGGAC
TCGCTCATCAACCTTCAGAACGGCATCAGGTCCCGCGACTACACGTCGGAAAGTGAAGAAAAG
AGGAATCGCTATCAT**TG**ACAAGGCAGGAACAGGGTGGCTGCAAGAGGCCTGTGCAATACATGT
ACATAGACCATATAAATATATATATATAAATATATATATATACAGAATATAAATATATATATT
ATATACAGATTTTAAAAAAGAGATAATGCCTATGTACCAGGGAGAAGGAGCGGGCCCTCCCGC
GCCCTGTGCTGGCCGGAGCAGCGTTTTCTTATGGTGGAGCAGCTGAGGAGGGCAGGAACCGCC
TCTCAGCACCGACCTCCCCTGATCTCCCTCCTCCACCCCTCTGTTCCCCACCCCTTCCCTTGC
TGGCCATTCTTGGCTTTTAGAAGGGAAATGTTGAGCCAAAGTTATGCCTGCGAAGACCCTAAG
GTCTCAAAAAGAAGTCTTAAGACGGCATTGCTTAAGGTGCTTCATTCCCTAATCCCCTTTTGA
TTTGTTTCCAAAATAAAGAGAATCTTTTCTCCCTAAAAA

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FIGURE 570

><subunit 1 of 1, 425 aa, 1 stop
><MW: 49786, pI: 8.84, NX(S/T): 3
MPTSSAVLLRVLSIPLLTVLILARDLSALGGCPWGPLPLRCHCLLPDPLFCAGEVQAFYE
DLSGRQYVNEVFNFSDKLYDLLFTNSPFQRDFMEQRRFSDIIFHPWKKEENGNSRVIL
YTITLTNPLAPKTATVRETQTMKASQSECEYVIDAEVLTHDVPYHDYFYTINRYTLTRV
ARNKSRLRVSTELRYRKQPWGLVKTFIEKNFWSGLEDFRHLSEELAKTESTYLAEMHRQ
SPKEKASKTTTVRRRKRPVHLRVPHLEEVMSPTTPTDEDVGHRIKHVAGSTQTRHIPE
DTPNGFHLQSVSKLLLVISCVLVLLVILNMMLFYKLWMLEYTTQTLTAWQGLRLQERLPQ
SQTEWAQLLESQQKYHDTLQKWREIIKSSVMLLDQMKDSLINLQNGIRSRDYTSESEEEK
RNRYH

Important features of the protein:**Signal peptide:**

Amino acids 1-28

Transmembrane domain:

Amino acids 312-334

N-glycosylation sites:

Amino acids 73-77;114-118;183-187

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 97-101

Tyrosine kinase phosphorylation sites:

Amino acids 144-153;188-196

N-myristoylation sites:

Amino acids 201-207;291-297

Leucine zipper pattern:

325-347

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FIGURE 571

GTAGAGAGTGAAGCAGCAAGACTGCAGAGCCTCATCAAGAAGTGTGGAGTGAAGGGAAGGCTTCAGATGGACAAT
TTGTGTGCTGGGGAAAAAATGGAATGTGCTGCAAATTCCTGTGGATAAGGGTGGACGGCTGCTCTGTCAACTT
TGACCATTTTCAGATTCTGCGGGCCATTGGTAAAGGGAGTTTTGGAAAGGTATGCATCGTGCAGAAGCGAGACAC
TAAGAAAATGTATGCAATGAAGTACATGAACAAGCAGAAGTGCATCGAGAGGGATGAGGTTCCGAATGTTTTCCG
GGAGCTGCAGATCATGCAAGGGCTGGAGCACCCCTTCCTGGTCAATCTGTGGTACTCCTTCCAGGATGAGGAGGA
CATGTTTCATGGTGGTGGACCTGCTCCTGGGAGGCGACCTGCGCTACCATCTGCAGCAGAATGTGCATTTACAGA
GGGACTGTGAACTCTACATCTGTGAGCTGGCACTGGCCCTGGAGTATCTTCAGAGGTACCACATCATCCACAG
AGACATCAAGCCAGACAATATCCTGCTGGATGAACACGGACATGTTACATTACAGACTTCAACATAGCGACGGT
AGTGAAGGAGCAGAAAGGGCTTCCTCCATGGCTGGCACCAAGCCCTACATGGCTCCAGAAGTATTCAGGTGTA
CATGGACAGAGGCCCCGGATACTCGTACCCTGTCGACTGGTGGTCCCTGGGCATCACAGCCTATGAGCTGCTGCG
GGGCTGGAGGCCGTACGAAATCCACTCGGTACGCCCCATCGATGAAATCCTTAACATGTTCAAGGTGGAGCGTGT
CCACTACTCCTCCACGTGGTGCAAGGGGATGGTGGCCCTGCTGAGGAAGCTCCTGACCAAGGATCCTGAGAGCCG
CGTGTCCAGCCTTCATGACATACAGAGCGTGCCCTACTTGGCCGACATGAACTGGGACGCGGTGTTCAAGAAGGC
ACTGATGCCCCGGCTTTGTGCCCAATAAAGGGAGGTTGAACTGCGATCCACATTTGAGCTTGAAGAGATGATTCT
AGAATCCAAGCCACTTCACAAAAAGAAGAAGCGATTGGCAAAGAACAGATCCAGGGATGGCACAAGGACAGCTG
CCCCCTGAATGGACACCTGCAGCACTGTTTGGAGACTGTCCGGGAGGAATTCATCATATTCAACAGAGAGAAGCT
CAGGAGGCAGCAGGGACAGGGCAGCCAGCTCTTGGACACCGACAGCCGAGGGGGAGGCCAGGCCCAAAGCAAGCT
CCAGGACGGGTGCAACAACAACCTCCTCACCCACACCTGCACCCGTGGCTGCAGCAGCTGAGCCCCACACTTGTG
CTGCTCAACAGGACTGCACTCGTCTCTGCCCTGCCACCCAGAGCCCCCTCTTTGTGCCCTGATGGTCCCTGTCTC
ACCCCTGAAAACATCAGATGCAGAAAAAGCCCTGGACTTGGAGCTGGGAAGCCTGGGTCTGGTCCCATCTCCAT
GACTGATTACGTGTGACCTCAGACAAGTCACGCCCTCTCTGTGCCTCCGTTTTCTGCATCTGCCAAAGGGGTTA
AACACTTCTGCCCCACTTCAAATTACAAGATTATGGGGAGAACCCAATTAGGTAGGAAACATGAAAAACCTTTGA
TATTTATAAAATCATTTTTTACGTGCAAAATATAACCTTAATATTTGAAGTGACCCCCATTCCCAAAGCAATCAA
ACCGTCATGACTTTGCAATTTGGCACATCCTAGCTTGTTAGAGGGCACTTCCGAAAAACACAGCCCTGACAGCAA
AATAAAGGTCTGATATGTTGGCCCCCTTCTATGGAAACAACGCTGCCAAATCCTGGAGCAAAACCTGAAGTGTCTT
CATGTGCATTCTCTGGCAGGCCACAGTCTTCTGAGCTTGTAAGATGGTGCAGCATGCAGACCAGACTTGTCCCC
AAGGTCTCAGCGCTGCGGTCTCACTCCTCCCTCATTTAAGAAGACTATCCTTACCTTTTAGTTTCAGCAGTCCT
CACCACCACCATATCCCAGTGCTGGGATGGCACACAGGTGTCCATTGAGATGAGAGTTGGGTGCTGAGCATTG
GTTACTCCTGCAGAGTGTAATCAGCACCCCATCCAAGTGGCCCGAAAGCCAGACCTGCAGCAGAAGTCTCCAAC
TCTCTATCAGCTTTCAGGGTTTTCTCTCCTGGGAAGGGTGTAAATCAGCTTGTGAGATTCTTCTTACAGAGAGT
ATCCAATCGGTATTGGTGGAGCGGCTCCCTATTTATAAATAGGAAGCATGGGTGCTTAGAAAGTTTATTTTCAAG
AGGAAAATGGGTTCACACAAAAAGCAAACCTACATTCTGATCTGCTCAGGGAGAAGCTTGCCTTTGAACTGGAAGA
TGTTGGGATGAGCAGGGAAAGCTTAGACTTTGGAGTCAAGTGTGTTTGAATCCAGCCCTGCTGGCTACTAAC
TAAGTGGGAGACCTTAGGCAAAGCATGCAATCGCTCTGAATGGCAGTTTCCCTCATTTTTTAAACAGGGATAATAAA
ACTAATATTGCAGGGGAGTTACAGGGTTAAATAAGATCCTGTGTGTAACCCCAAGCATTGGATGACTCATAGAAT
GGCCTTTTTTGTGAGCATAATCGTCATCATTATTTAGATACTTTCTTCCCTCACTCACCCAGCAGGTGAGTTTTT
TGTGCAACAAACCTGTTTAGGATTCTTCCAAATGTTCTTCCCTGGGGTCTTTGATATTTGTTTGTACATCCTGC
TGAAGTTCGACTGTGTTTTTATTTTTTCATCCAACTTCCATTTTTTCACTTTTTTACATGATTACTCAATCCTTGGG
GCTGTCCATGTCATCTCTTAGATTTCTTAAAAGACATTTTAATGTATGGTTAGGTTTTATATTTTTATTTTTTAA
AAAAGAAATAGTCAGTGTTCCTCCTTTCAACCGAGACTATTTCTGGATTGTGTGCTCCTCGTCAGTTGACTTGT
TTTGACACTTTTTCTTTACTTCATGTCCCATCAACAACCGTCCTGCTCCCCACCTCCCCCAGGAAATAAGGGGC
CTGCTCCTCTCCCTACTGTGACCCCTGGAGGCTCTTAAGATGATGATGGTTTTTTTTATTTGGGCTGAGTTCAGAA
TTAGGGGCAGGAGCTGGAAGTCGCCCTAGGAACACCAGATTTCTGGTTCGTGTTCAAGTTGGCATTTCTTGTGTTG
GAATAAACTATTTCTTGG

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FIGURE 572

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA136110
<subunit 1 of 1, 364 aa, 1 stop
<MW: 42195, pI: 7.40, NX(S/T): 1
MKYMNKQKCIERDEVNRNVEFRELQIMQGLEHPFLVNLWYSFQDEEDMEMVVDLLLGGDLRY
HLQQNVHFTEGTVKLYICELALALEYLQRYHIIHRDIKPDNILLDEHGHVHITDFNIATV
VKGAERASSMAGTKPYMAPEVFQVYMDRGPYSPVDWWSLGITAYELLRGWRPYEIHVS
TPIDEILNMFKVERVHYSSTWCKGMVALLRKLLTKDPESRVSSLHDIQSVPYLADMNWDA
VFKKALMPGFVPNKGRLNCDPTFELEEMILESPLHKKKKRLAKNRSRDGTDSCPLNGH
LQHCLETVREEFIIFNREKLRRQQGQGSQQLDTSRGGGQAQSKLQDGCNNNLLTHTCTR
GCSS

Important features of the protein:**N-glycosylation site:**

Amino acids 285-289

N-myristoylation sites:

Amino acids 123-129;290-296;337-343;339-345;348-354

Serine/Threonine protein kinases active-site signature:

Amino acids 92-105

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FIGURE 573

CTCCAGTTCGCCGACTGTAACATGTTTCATCCAGTTCAGTATGTTTTGTATGCAAGTTGGAAATAAATAAACGTC
CTGAACTGGATGAAACATGTTACAGTCGGCCGAAACATGAGAGGCTGTGTGAGAAGCTGCAGCCGCCGGCAGAGG
AGACCTCAGCATCATCTAGAGCCCAGCGCTGGCCCTGCCCTCCGCCCTGCCCGCCGCCGCCGTCGCCGTTTCTGTT
CCTGCTACTGTCCCACCTAAACAACCTCCCGTTACACGGACAAGTGAACATCTGTGGCTGTCCTCTCCTTTTCTTC
CTCCTCTTCCAACTCCTTCTCCTCCTCCCACTTCCCAGCCGCAGCAGAAAGCCCCCAACCAACTGACGCTGGCA
CAACTGCAAACGGTGTCTATCCGCACAACCTTTATCTCGCTCCTCGGGCTCCCCTAAGGCATTGGACCCATCGCCGC
GTCTTTTATTTTGCAAAGTTGCATCGCTGTACATATTTTGTCCCCGCCACCTCCCTCTGTCTCTGGAGTGCCC
TACAGCCCCGCAAACTCCTCCTGGAGCTGCGCCCTAGTGCCCCCTGCTGGGCGAGTGGCGTTCCCCCCCATCCTCCC
GCGCCCAGCCCCCTGCTGCTCTGGGCAGACGATGCTGAAGATGCTCTCCTTTAAGCTGCTGCTGCTGGCCGTGGCT
CTGGGCTTCTTTGAAGGAGATGCTAAGTTTGGGGAAGAAACGAAGGGAGCGGAGCAAGGAGGAGAAGGTGCCTG
AATGGGAACCCCCCGAAGCGCCTGAAAAGGAGAGACAGGAGGATGATGTCCCAGCTGGAGCTGCTGAGTGGGGGA
GAGATGCTGTGCGGTGGCTTCTACCTCGGCTGTCTGCTGCCTGCGGAGTGACAGCCCGGGGCTAGGGCGCCTG
GAGAATAAGATATTTTCTGTTACCAACAACACAGAATGTGGGAAGTTACTGGAGGAAATCAAATGTGCACTTTGC
TCTCCACATTCTCAAAGCCTGTTCCACTCACCTGAGAGAGAAGTCTTGAAAGAGACCTAGTACTTCCTCTGCTC
TGCAAAGACTATTGCAAAGAATTCTTTTACACTTGCCGAGGCCATATTCCAGGTTTCTTCAAACAACCTGCGGAT
GAGTTTTGCTTTTACTATGCAAGAAAAGATGGTGGGTTGTGCTTTCCAGATTTTCCAAGAAAACAAGTCAGAGGA
CCAGCATCTAACTACTTGGACCAGATGGAAGAATATGACAAAGTGGAAGAGATCAGCAGAAAGCACAAACACAAC
TGCTTCTGTATTTCAGGAGGTTGTGAGTGGGCTGCGGCAGCCCGTTGGTGCCCTGCATAGTGGGGATGGCTCGCAA
CGTCTCTTCATTCTGGAAGAAAGAGGTTATGTGAAGATACTTACCCCTGAAGGAGAAATTTTCAAGGAGCCTTAT
TTGGACATTCACAACTTGTTCAAAGTGGAATAAAGGGAGGAGATGAAAGAGGACTGCTAAGCCTCGCATTCAT
CCCAATTACAAGAAAATGGAAAGTTGTATGTGTCTTATACCACCAACCAAGAACGGTGGGCTATCGGGCCTCAT
GACCACATTCTTAGGGTTGTGGAATACACAGTATCCAGAAAAAATCCACACCAAGTTGATTTGAGAACAGCCAGA
GTCTTTCTTGAAGTTGCAGAACTCCACAGAAAGCATCTGGGAGGACAACCTGCTCTTTGGCCCTGACGGCTTTTG
TACATCATTCTTGGTGATGGGATGATTACACTGGATGATATGGAAGAAATGGATGGGTAAAGTATTTTACAGGC
TCAGTGCTACGGCTGGATGTGGACACAGACATGTGCAACGTGCCTTATTCATACCAAGGAGCAACCCACACTTC
AACAGCACCAACCAGCCCCCGAAGTGTTGCTCATGGGCTCCACGATCCAGGCAGATGTGCTGTGGATAGACAT
CCCACTGATATAAACATCAATTTAACGATACTGTGTTACAGACTCCAATGGAAAAACAGATCATCAGCCAGAATT
CTACAGATAATAAAGGGGAAAGATTATGAAAGTGAGCCATCACTTTTAGAATTCAAGCCATTCAGTAATGGTCCT
TTGGTTGGTGATTTGTATACCGGGGCTGCCAGTCAGAAAGATTGTATGGAAGCTACGTGTTTGGAGATCGTAAT
GGGAATTTCTAACTCTCCAGCAAAGTCCTGTGACAAAGCAGTGGCAAGAAAAACCACTCTGTCTCGGCACTAGT
GGGTCTGTAGAGGCTACTTTTCCGGTCACATCTTGGGATTTGGAGAAGATGAAC TAGGTGAAGTTTACATTTTA
TCAAGCAGTAAAAGTATGACCCAGACTCACAATGGAAAACTCTACAAAATTGTAGATCCCAAAAGACCTTTAATG
CCTGAGGAATGCAGAGCCACGGTACAACCTGCACAGACACTGACTTCAGAGTGCTCCAGGCTCTGTGAAACGGC
TACTGCACCCCCACGGGAAAGTGCTGCTGCAGTCCAGGCTGGGAGGGGGACTTCTGCAGAACTGCAAAATGTGAG
CCAGCATGTGTCATGGAGGTGTCTGTGTTAGACCGAACAAGTGCCCTCTGTAAAAAAGGATATCTTGGTCCTCAA
TGTGAACAAGTGGACAGAAACATCCGCAGAGTGACCAGGGCAGGTATTCTTGATCAGATCATTGACATGACATCT
TACTTGCTGGATCTAACAAGTTACATTGTATAGTTTCTGGGACTGTTTGAATATTCTATTCCAATGGGCATTTAT
TTTTTATCCTGTCAATTAATAAAAAAAAAAAGACTGTTATCCTGCTACACACTCCTGTGATTTCAATTCTCTTTTATTAA
TTTAAAAATAATTTCCAGAAATGTGCAGATCCTCTGTGTGTATGTCAGCATGTTTGTTCACATATGCACATACAC
ATACTCATAACCCCTATATGCGTTGTTGCATAACAGATGATTTTTTTAAATATATACTTCCTTATGCAAAGTAAT
TTACACAGAAATTCATTGTAAATTGATAATGGATTTTTTATGTTACTAGAAGAGATTATTTGACTTCCCAGGAA
TTTTCTGTCTGTAATCACTAAAGTCAACTTTAATAGAGTTTTGAAACAGTACTGTGCAATCCGATGGATCTAATT
AAAAAAAAGGCAATATTTTTTATATTAAAGTACTATACTAGGAGAGAATGTTTCAGAACTCCCTGATGAATTTCTA
AGTGAGCAACTTGATATAAAATTGTAATCTTCATTTTTGTGAGTGATCCAGTTACAGAATGCTACACACTTACC
TTTTTATTGGCTGAGAAATCTGGTTATTTTCATCTTAATCTCAAGATTGTTTTCAAGTGTTTTATAATTAAATCAT
AATAGCATATTTTAAATCAAAAA

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FIGURE 574

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139592
><subunit 1 of 1, 882 aa, 1 stop
><MW: 98428, pI: 8.89, NX(S/T): 5
MKHVTVGRNMRGCVRSCSRQRRPQHHLEPSAGPASACAAAVAVSVPATVPPKQLPLHG
QVNICGCPLLFFLLFQLLLLLLPLPSRSRKPTQLTLAQLQTVSSAQLYLAPRAPLRHWTH
RRVFYFCKVASLYIFLSPPPPSVSGVPYSPANSSWSCALVPLLGSVPPHPPAPSPCCSG
QTMLKMLSFKLLLLLAVALGFFEGDAKFGERNEGSGARRRRCLNGNPPKRLKRRDRRMMSQ
LELLSGGEMLCGGFYPRLSCLLSDSPGLGRLENKIFSVTNNTTECGKLLEEIKCALCSPH
SQSLFHSPEREVLERDLVLPLLCKDYCKEFFYTCTRGHIPGFLQTTADEFCFYARKDGGL
CFPDFPRKQVRGPASNYLDQMEEDYDVEEISRKHKHNCFCIQEVVSGLRQPVGALHSGDG
SQRLFILEKEGYVKILTPEGEIFKEPYLDIHKLVSQGIKGGDERGLLSLAFHPNYKKNKG
LYVSYTTNQERWAIGPHDHILRVVEYTVSRKNPHQVDLRTARVFLEVAELHRKHLGGQLL
FGPDGFLYIILGDGMITLDDMEEMDGLSDFTGSVLRLDLDVDTMCNVPYSIPRSNPHFNST
NQPPFVFAHGLHDPGRCAVDRHPTDININLTILCSDSNGKNRSSARILQIIKGKDYSEF
SLLEFKPFSSNGPLVGGFVYRGCQSERLYGSYVFGDRNGNFLTLLQOSPVTQWQEKPLCLG
TSGSCRGYFSGHILGFGEDELGEVYILSSSSKSMQTTHNGKLYKIVDPKRPLMPPEECRATV
QPAQTLTSECSRLCRNGYCTPTGKCCSPGWEGDFCRTAKCEPACRHGGVCVRPNKCLCK
KGYLGPQCEQVDRNIRRVTRAGILDQIIDMTSYLLDLTSYIV

Important features of the protein:**Transmembrane domains:**

Amino acids 63-80;186-201

N-glycosylation sites:

Amino acids 152-156;281-285;598-602;629-633;641-645

Glycosaminoglycan attachment site:

Amino acids 417-421

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 856-860

N-myristoylation sites:

Amino acids 12-18;413-419;457-463;698-695;720-726;723-729

EGF-like domain cysteine pattern signatures:

Amino acids 805-817;837-849

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FIGURE 575

CGGCTCGAGAGCGGGGCAAACCTGCTTGGCACCTCTTCAATAGGTGACATTCAATGATAGATCT
CTGGCTTCCTGCTCTGTTTGTCTGGTTGCCCTGGAAAGCCTGCTGCTCAGCCCATGCCCCGG
GACTTCCTCCACCCTCACCAGGACATTCTTTCCATCTCTTGTCTCCTGTGTGCAAGTCCCTTT
CTCCTGGATTCCATGTCTTGAATGTTTCTTAATTTACTTCCTCATTTTGGCAGAGGATGTCCT
CCAGTTGTTTTCTGGGAATGCTAATATGCAAGTGAACCAGTGACCTGCAGTTCTGCCCACACA
GGGTTAATAACCAATCAGATTCTCTCTTTTCAAGATGGTTAACATAACAGACACCAAGAAAGG
GAAGAGGAGCCGACAGCAGAGGGGGGAAGCTGAAAAGACGCACAAAGAATGGCCATAAAAGATA
TGAGCAACCCCAGCTTTCCAGACAGTCACTTTTCCAGTGGTCATACCTGGTCTGGAAGATTCT
CCCATCATCTCGAATAAAGCTGTTGTTGCTTTTAACTCCATGGAGAGACCGAATGGAGTGAGC
CCAGCAGGGCATGCTGGGCAAGAGAGGTCCCCCGAGTCCCAAATAAGAATTTCAACTAGTATA
AAACGAGGCAGCGAACCCACACGTGGAAGTCTGATACCGCTTGCAGAAGGGAATTGAATAGAT
GTCTCCCTATTGGTAAGGATGTGGTTTTATTGACTTGAAATAACAAAGCCCGCAAGCAACAAC
TGATCATCCGCGGGATGCTGCCACAAGGAATAATTGAGCACTCATTCAGACACAGGGGAAACC
ACTGCCTCTTTCAGTCTTTCTCCAGATTCCAACAGTCAGTGTTACAGCATTTCACCTTGTTT
ACCTCCCTGAGAAGACGTTGCAGCTCACTCACCCAGTGGGCACTGGGAGCCTCTGCTCAGGT
GGGAGACAGATGCCCCCCACATGCACATCTGGTGTATTATGAAGCAGATACTGGGGCTTCATAA
ACACAGAAGGGGCGAGGAAGTAGCCCCAGGGCATAGTGTGGGGCCTCCTGACTAAAAGTAGCTT
GCAAACCCCTGCCTATAACAGCCACTTCCTGGCAGTCATTGTGCCACTTAGGAGCCCTCCTCA
CCGCTCTTCCTTTAGTTTCCTTCACTCTGTATAGACCTGCCAGAGCAGCTCAGGGTGGAGCAG
CTGCAGCCATGGGACCTGCTCCAGGCAAGGCCCTATGCTACACAGTCCCTGGGGGTGAGGATT
CCAGAGGAGTCAATTCCCTACCCGCCCTTCCAGGGGATGGCCGAGATGAGCGTTCCACAGGG
AAAGTGAAAGTTGCAAGGCTGTTGCGGAAACACCAGGGGTTCATTTAGGTCTTGCTGCTCAT
CTCACAGAAAGCCAGTCACTGAGACAAGTATTGTCAGGGAAGAAGGCTTTATCCAGGTGCTAC
AGACAGGGTGAACAAGAGATCAGTCTCAAATCCATCATCAACTGACTAAAATTAGGGGTT
TATATAGCAGGGAAGAAATGTAACCTACATGTGGGAAAACAGGGATTAACGAGGGGCAAGGAAG
AGGAGTTGGCCAACAGGCAGCAGGTGGTCACCTGGGGAATCATGATGGGTGAGGGGTCTGGCT
TCTCACTTTCCAGATGTGGGGATCTGGTAAATTTTCACTTTCTTGATAACCGTCTGGGAGGATTG
CTGGCTGGTTTCCTGAGAAAGGAATTCAGATGACATAAATGTAAATTTCTCCTTGGGTTTCAA
GACTGAGAGGGTCAATTTCTAGGTTTATTCAAGAAAAACCATAAACATCAGTTCTATGGGACA
ATTGGGCCCATTTCAGGCTCTGAGGATAAGGGTTAATGAGGGGACAGAGTCGCCTGGAGAAG
TTCCTGAGGGCCTACAAGAACTAGAGAGGCTTCCTGGCAAAGCTCTATGCTGTCTATCCTCT
CTTCTCTCCTTGACAGGAAGATTCCAGTATAATAGACCCGAGGTGAAAAGGCTTTTGTTCATA
AGTAGAAAACCTGAAGGGGGGTGGGAGGCACATGGATTTGAACCAGAGACCGCTTGGCCTGCAG
GCAAATGCTGTACCTTCAGTTGCACCCCTCACTTGTTACAGCTGTTTCTGATAAGCACTTGTC
CAGCCCCATCAGCACCTCGATTTCTTCTTGGTGAGTCCATGGGAACAGCCCCACTGCAAACAA
CCCATTCCTGCTCTCCTCTTTCTCTAAACCTCAACCTCCTCCTACCTGGCAGTCCACAGGCC
TACAGCTTCTCCTCAGTGGGAAAGACATCAGCTTGGAAAACCACTTGGAAAGCCAACGTTATC
CTAGAAAAGCTTTTTTAAATGACCCAGCAGGACAAGTCTCCGGATGGCCTTGGCCAACCCGGTG
CTTCCCTCTTTTCTTGGTTGTAGTTCTCAGAATAACTAGAGAATGTACTGGGAGTGTTGTCT
GAGATAAGGAGGAACTGTCCTAAACCTGGACTCTGTTCCCATCACACCTAGAACAGGATGTCC
TGCAACGCTTTAGCCCAATGATCCAAGTTGCCCTTGGGGTATAAACTTGACAGCAGAGGGCG
TTCAGGGTCCCTCAGCTGCAGTGTGAAGTGGGACACACAGGTGAGACTCCATCTGCCCTGGGC
AGGTTCTGAGCCTTGGGGGACCAGTTCACCCCTACATCCCAGGCTTCTGTTGTCCCTTGCCTG
CCTGTAAGGAATAAAGTTGCTTTGCTTA

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FIGURE 576

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA139608
><subunit 1 of 1, 80 aa, 1 stop
><MW: 8927, pI: 3.77, NX(S/T): 0
MIDLWLPALEFVLVALESLLLSPCPGTSSTLRTFFPSLVSCVQVPFSWIPCLECFLIYFL
ILAEDVLQLEFSGNANMQVNQ

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domain:

Amino acids 47-62

N-myristoylation sites:

Amino acids 25-31

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FIGURE 577

ATCGGTTAGCGCCTTGCCATGATTAATCCAGAGCTGCGGGATGGCAGAGCTGATGGCTTCATA
CATCGGATAGTTCCCAAGTTGATACAAAACCTGGAAGATTGGCCTTATGTGCTTCCTGAGTATT
ATTATTACTACAGTTTGCATTATTATGATAGCCACATGGTCCAAGCATGCTAAACCTGTGGCA
TGTTTCAGGGGACTGGCTTGGAGTGAGAGATAAGTGTTTCTATTTTTCTGATGATACCAGAAAT
TGGACAGCCAGTAAAATATTTTGTAGTTTGCAGAAAGCAGAACTTGCTCAGATTGATACACAA
GAAGACATGGAATTTTTGAAGAGGTACGCAGGAACCTGATATGCACTGGATTGGACTAAGCAGG
AAACAAGGAGATTCTTGGAATGGACAAATGGCACCACATTCAATGGTTGGCCATCAAACCTCC
AAATGGTCTTGCAACTGGAGCCTCCGACAATGGCTTCTTCTGCTGGGACCCCTTAGATAGGCC
TCTGAGGGAGCTCTGACTGCCGTTTCCCCAAAACAATGTCCCCTGTCAGCAGGAAGCAGTTAA
ATCAGTCTTCATCCTTATCCTTAATATAACGGCAGTTAGATGTACTTCTTTAGAGGGAGTAAA
TTTATCAATTCAGAGCAATTCATCCTCCTCTTTCCATCTTTGATTCACAGTTAATAGGCTATA
AATTTTGATAATGTAGAATAAACTACAGAAAACCTTCTTG

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FIGURE 578

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143292
><subunit 1 of 1, 160 aa, 1 stop
><MW: 18576, pI: 9.29, NX(S/T): 3
MINPELRDGRADGFIHRIVPKLIQNWKIGLMCFLSIIITTVCIIMIATWSKHAKPVACSG
DWLGVRDKCFYFSDDTRNWTASKIFCSLQKAELAQIDTQEDMEFLKRYAGTDMHWIGLSR
KQGDSWKWTNGTTFNGWPSNSKWSCNWSLRQWLLLLGPLR

Important features of the protein:**Signal peptide:**

Amino acids 1-42

N-glycosylation sites:

Amino acids 78-82;130-134;146-150

N-myristoylation site:

Amino acids 131-137

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FIGURE 579

TGAAGGCCTGTGAGTGAGGAATGCCTCTCACCAGCTGTGCCTGAGCTGCAGCACTCCAGCCAC
TGCTGTCTCCTTAGCTGCTCACAT**ATG**GATACTTTCACAGTTCAGGATTCCACTGCAATGAGC
TGGTGGAGGAATAATTTCTGGATCATCTTAGCTGTGGCCATCATTGTTGTCTCTGTGGGCCTG
GGCCTCATCCTGTACTGTGTCTGTAAGTGGCAGCTTAGACGAGGCAAGAAATGGGAAATTGCC
AAGCCCCTGAAACACAAGCAAGTAGATGAAGAAAAGATGTATGAGAATGTTCTTAATGAGTCG
CCAGTTCAATTACCGCCTCTGCCACCGAGGAATTGGCCTTCTCTAGAAGACTCTTCCCCACAG
GAAGCCCCAAGTCAGCCGCCCCGCTACATACTCACTGGTAAATAAAGTTAAAAATAAGAAGACT
GTTTCCATCCCAAGCTACATTGAGCCTGAAGATGACTATGACGATGTTGAAATCCCTGCAAAT
ACTGAAAAAGCATCATTT**TGA**AACAGCCATTTCTTCTTTTGGCAAACTGAAGAGGGTTCAC
ACAACCTATTTTAAAACAATCAAGAATGGTTGAACTTCAGTAGGTCTCTGGGCCCTGAAAGCC
AGTGGTGATTTTATGAAGCTCTATAAGATAAAGCACTTCCCAAACCTTAGATGAAGACACCCC
TGCGATCGGATGACTGCAGCCAGAGGAGACACATGGGTGCTCGGCTCTGAGGACTTAGAGGGG
TCAGCCTTGTGCTGTTGAGGAACTTTCCATGGGAAGGACCACGGGGCTCCATGGCTCCCACC
TGTGGGAACTACTCATTTCTTGGCATTCCTTCCCCCTTCATTCCCTTTGGTTTGCATGGTTC
TGAGTGATATTAAATCTCAGCATTTGGTTGTGCAAAAAAAAAA

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FIGURE 580

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144844
><subunit 1 of 1, 145 aa, 1 stop
><MW: 16618, pI: 5.26, NX(S/T): 1
MDTFTVQDSTAMSWWRNNFWIILAVAIIVSVGLGLILYCVCKWQLRRGKKWEIAKPLKH
KQVDEEKMYENVLNE SPVQLPPLPPRNWPSLEDSSPQEAPSQPPATYSLVNKVKNNKKTVS
IPSYIEPEDDYDDVEIPANTEKASF
```

Important features of the protein:**Signal peptide:**

Amino acids 1-35

Tyrosine kinase phosphorylation site:

Amino acids 61-70

Amidation site:

Amino acids 48-52

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FIGURE 581

GGCCGCCTCCGCGGGGCTGTGGGAAGCTTGGGCTGTCCCAGGACCGTCAGTCTCCTCCTCTGA
CCCTCCCTTTCCCCTTGTGTGTAGGGCCGCGTCCCACCCCCACCTCGCCGGAGTCCGGGGCG
GCCCCGGTGTCCCCTCCGAGCCTGCTGCACTCCACGTCCCCCTACCAGGGCTCCAGCCCCCAG
GGAAATCTCCGACCAGGCCCGCCCAGGAGCCAGATCCAGGCTCCTGGAAGAACCATGTCCGGC
AGCTACTGGTCATGCCAGGCACACACTGCTGCCCAAGAGGAGCTGCTGTTTGAATTATCTGTG
AATGTTGGGAAGAGGAATGCCAGAGCTGCCGGCTGAAAATTACCCAACCAAGAGAAATCTGCAGG
ATGGACTTTCTGGTCCTCTTCTTGTCTACCTGGCTTCGGTGCTGATGGGTCTTGTTCTTATC
TGCGTCTGCTCGAAAACCCATAGCTTGAAAGGCCTGGCCAGGGGAGGAGCACAGATATTTTCC
TGATAAATTCAGAATGTCTTCAGAGAGCCGTGCATGGATTGCTTCATTACCTTTTCCATACG
AGAAACCACACCTTCATTGTCCTGCACCTGGTCTTGCAAGGGATGGTTTATACTGAGTACACC
TGGGAAGTATTTGGCTACTGTCAGGAGCTGGAGTTGTCCTTGCATTACCTTCTTCTGCCCTAT
CTGCTGCTAGGTGTAAACCTGTTTTTTTTTACCCTGACTTGTGGAACCAATCCTGGCATTATA
ACAAAAGCAAATGAATTATTATTTCTTCATGTTTATGAATTTGATGAAGTGATGTTTCCAAAG
AACGTGAGGTGCTCTACTTGTGATTTAAGGAAACCAGCTCGATCCAAGCACTGCAGTGTGTGT
AACTGGTGTGTGCACCGTTTCGACCATCACTGTGTTTGGGTGAACAACTGCATCGGGGCCTGG
AACATCAGGTACTTCCTCATCTACGTCTTGACCTTGACGGCCTCGGCTGCCACCGTCGCCATT
GTGAGCACCACTTTTCTGGTCCACTTGGTGGTGATGTCAGATTTATACCAGGAGACTTACATC
GATGACCTTGGACACCTCCATGTTATGGACACGGTCTTTCTTATTCAGTACCTGTTCTGACT
TTTCCACGGATTGTCTTCATGCTGGGCTTTGTCGTGGTTCTGAGCTTCCTCCTGGGTGGCTAC
CTGTTGTTTGTCTGTATCTGGCGGCCACCAACCAGACTACTAACGAGTGGTACAGAGGTGAC
TGGGCCTGGTGCCAGCGTTGTCCCCTTGTGGCCTGGCCTCCGTCAGCAGAGCCCCAAGTCCAC
CGGAACATTCACCTCCCATGGGCTTCGGAGCAACCTTCAAGAGATCTTTCTACCTGCCTTTCCA
TGTCATGAGAGGAAGAAACAAGAATGACAAGTGTATGACTGCCTTTG

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FIGURE 582

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA144857
><subunit 1 of 1, 344 aa, 1 stop
><MW: 39787, pI: 7.44, NX(S/T): 2
MDFLVLFYFLASVLMGLVLICVCSKTHSLKGLARGGAQIFSCIIPECLQRAVHGLLHYL
FHTRNHTFIVLHLVLQGMVYTEXTWEVFGYCQELELSLHYLLLPYLLLGVNLFFFTLTCG
TNPGIITKANELLFLHVYEFDEVMFPPKNVRCSTCDLRKPARSKHCSVCNWCVHRFDHHCV
WVNNCIGAWNIRYFLIYVLTLTASAATVAIVSTTFLVHLVVMSDLYQETYIDDLGHLHVM
DTVFLIQYLFLETFPRIVFMLGFVVVLSFLLGGYLLFVLYLAATNQTTNEWYRGDWAWCQR
CPLVAWPPSAEPQVHRNIHSHGLRSNLQEIFLPAFPCHERKKQE

Important features of the protein:**Signal peptide:**

Amino acids 1-29

Transmembrane domains:

Amino acids 100-116;201-217;256-275

N-glycosylation sites:

Amino acids 65-69;284-290

N-myristoylation sites:

Amino acids 32-38;77-83;120-126;322-328

Cell attachment sequence:

Amino acids 292-298

DHHC zinc finger domain:

Amino acids 140-204

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FIGURE 583

CCGCGGAACCTGGCAGGCGTTTCAGAGCGTCAGAGGCTGCGGATGAGCAGACTTGGAGGACTCCAGGCCAGAGACT
AGGCTGGGCGAAGAGTCGAGCGTGAAGGGGGCTCCGGGCCAGGGTGACAGGAGGCGTGCTTGAGAGGAAGAAGTT
GACGGGAAGGCCAGTGCGACGGCAAATCTCGTGAACCTTGGGGGACGAATGCTCAGGATGCGGGTCCCCGCCCTC
CTCGTCCTCCTCTTCTGCTTCAGAGGGAGAGCAGGCCCGTCGCCCCATTTCTGCAACAGCCAGAGGACCTGGTG
GTGCTGCTGGGGGAGGAAGCCCGGCTGCCGTGTGCTCTGGGCGCCTACTGGGGGCTAGTTCAGTGGACTAAGAGTGGG
CTGGCCCTAGGGGGGCCAAAGGGACCTACCAGGGTGGTCCCGGTACTGGATATCAGGGAATGCAGCCAATGGCCAG
CATGACCTCCACATTAGGCCCGTGGAGCTAGAGGATGAAGCATCATATGAATGTCAGGCTACACAAGCAGGCCTC
CGCTCCAGACCAGCCCAACTGCACGTGCTGGTCCCCCAGAAGCCCCCAGGTGCTGGGCGGCCCTCTGTGTCT
CTGGTTGCTGGAGTTCCTGCGAACCTGACATGTCGGAGCCGTGGGGATGCCCCGCCCTACCCCTGAATTGCTGTGG
TTCCGAGATGGGGTCTGTGGATGGAGCCACCTTTCATCAGACCCTGCTGAAGGAAGGGACCCCTGGGTGCTG
GAGAGCACCTTAACCCCTGACCCCTTTCAGCCATGATGATGGAGCCACCTTTGTCTGCCGGGCCCGGAGCCAGGCC
CTGCCACAGGAAGAGACACAGCTATCACACTGAGCCTGCAGTACCCCCAGAGGTGACTCTGTCTGCTTCGCCA
CACACTGTGCAGGAGGGAGAGAAGGTCATTTTCCTGTGCCAGGCCACAGCCAGCCTCCTGTACAGGCTACAGG
TGGGCAAAGGGGGCTCTCCGGTGCTCGGGGCCCGGGCCAAGGTTAGAGGTCGTGGCAGACGCCTCGTTCTG
ACTGAGCCCGTGTCTGCGAGGTCAGCAACGCCGTGGGTAGCGCCAACCGCAGTACTGCGCTGGATGTGCTGTTT
GGGCCGATTCTGCAGGCAAAGCCGGAGCCCGTGTCCGTGGACGTGGGGGAAGACGCTTCCTTCAGCTGCGCCTGG
CGCGGGAACCCGCTTCCACGGGTAACTGGACCCGCCCGGCTGGCGCGCAGGTGCTGGGCTCTGGAGCCACACTG
CGTCTTCCGTCCGTGGGGCCCCGAGGACGCAGGCGACTATGTGTGCAGAGCTGAGGCTGGGCTATCGGGCCTGCGG
GGCGGCGCCGCGGAGGCTCGGCTGACTGTGAACGCTCCCCAGTAGTGACCGCCCTGCACTCTGCGCCTGCCTTC
CTGAGGGGCCCTGCTCGCCTCCAGTGTCTGGTTTTTCGCCTCTCCCGCCCCAGATGCCGTGGTCTGGTCTTGGGAT
GAGGGCTTCTGGAGGCGGGGTGCGAGGGCCGGTTCCTGGTGGAGACATTCCCTGCCCCAGAGAGCCGCGGGGA
CTGGGTCCGGGCCCTGATCTCTGTGCTACACATTTCCGGGGACCCAGGAGTCTGACTTTAGCAGGAGCTTTAACTGC
AGTCCCCGGAACCGGCTGGGCGAGGGAGGTGCCAGGCCAGCCTGGGCCGTAGAGACTTGCTGCCCACTGTGCGG
ATAGTGGCCGGAGTGGCCGCTGCCACCACAACCTCTCCTTATGGTCATCACTGGGGTGGCCCTCTGCTGCTGGCGC
CACAGCAAGGCCTCAGCCTCTTTCTCCGAGCAAAAGAACCTGATGCGAATCCCTGGCAGCAGCGACGGCTCCAGT
TCACGAGGTCTGAAGAAGAGGAGACAGGCAGCCGCGAGGACCGGGGCCCATTTGTGCACACTGACCACAGTGAT
CTGGTTCTGGAGGAGGAAGGGACTCTGGAGACCAAGGACCCAACCAACGGTTACTACAAGSTCCGAGGAGTCAGT
GTGAGCCTGAGCCTTGGCGAAGCCCTGGAGGAGGTCTCTTCTGCCACCACCCTCCCCCTTGGGCCCCAGGG
ACCCCTACCTTCTATGACTTCAACCCACACCTGGGCATGGTCCCCCCTGCAGACTTTACAGAGCCAGGGCAGGC
TATCTCACCACACCCACCCCTCGAGCTTTCACCAGCTACATCAAACCCACATCCTTTGGGCCCCAGATCTGGCC
CCCGGGACTCCCCCTTCCCATATGCTGCCTTCCCCACACCTAGCCACCCGCGTCTCCAGACTCACGTGTGACAT
CTTTCCAATGGAAGAGTCCTGGGATCTCCAACCTGCCATAATGGATTGTTCTGATTTCTGAGGAGCCAGGACAAG
TTGGCGACCTTACTCCTCCAAACTGAACACAAGGGGAGGGAAAGATCATTACATTTGTCAGGAGCATTTGTATA
CAGTCAGCTCAGCCAAAGGAGATGCCCCAAGTGGGAGCAACATGGCCACCCAATATGCCACCTATTCCCCGGTG
TAAAGAGATTCAAGATGGCAGGTAGGCCCTTTGAGGAGAGATGGGGACAGGGCAGTGGGTGTTGGGAGTTTGGG
GCCGGGATGGAAGTTGTTTCTAGCCACTGAAAGAAGATATTTCAAGATGACCATCTGCATTGAGAGGAAAGGTAG
CATAGGATAGATGAAGATGAAGAGCATAACAGGCCCCACCCTGGCTCTCCCTGAGGGGAACTTTGCTCGGCCAAT
GGAAATGCAGCCAAGATGGCCATATACTCCCTAGGAACCCAAAATGGCCACCATCTTGATTTTACTTTCTTAAA
GACTCAGAAAGACTTGGACCCAAGGAGTGGGGATACAGTGAGAATTACCACTGTTGGGGCAAAATATTGGGATAA
AAATATTTATGTTTAAATAATAAAAAAAGTCAAAGAGAAAAAAA

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FIGURE 584

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145841
><subunit 1 of 1, 708 aa, 1 stop
><MW: 75093, pI: 6.65, NX(S/T): 3
MLRMRVPALLVLLFCFRGRAGPSPHFLQOPEDLVVLLGEEARLPCALGAYWGLVQWTKSG
LALGGQRDLPGWSRYWISGNAANGQHDHIRPVELEDEASYECQATQAGLSRPAQLHVL
VPPEAPQVLGGPSVSLVAGVPANLTCRSRGDARPTPELLWFRDGVLLDGATFHQTLLKEG
TPGSVESTLTLPFSHDDGATFVCRARSQALPTGRDTAITLSLQYPPEVTLSASPHTVQE
GEKVIFLCQATAQPPVTGYRWAKGGSPVLGARGPRLEVADASFLETPVSCEVSNAVGSA
NRSTALDVLFGPILQAKPEPVSVVDVGEDASFSCAWRGNPLPRVTWTRRGAQVLGSGATL
RLPSVGPEDAGDYVCRAEAGLSGLRGGAEEARLTVNAPPVVTALHSAPAFLRGPARLQCL
VFASPAPDAVVWSWDEGFLEAGSQGRFLVETFPAPESRGGLGPGGLISVLHISGTQESDFS
RSFNCSARNRLGEGGAQASLGRDLLPTVRIVAGVAAATTTLLMVITGVALCCWRHASKAS
ASFSEQKNLMRIPGSSDGSSSRGPPEEEETGSREDRGPIVHTDHSDLVLEEEGTLETKDPT
NGYYKVRGVSVSLSLGEAPGGGLFLPPPSPLGPPGTPTFYDFNPHLGMVPPCRLYRARAG
YLTPHPRAFTSYIKPTSFGPPDLAPGTPPPFYAAFPPTPSHPRLQTHV
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 511-531

N-glycosylation sites:

Amino acids 143-147;301-305;484-488

N-myristoylation sites:

Amino acids 48-54;60-66;79-85;139-145;180-186;183-189;355-361;383-389;
387-393;460-466;473-479;494-500;495-501;514-520;528-534;
554-560;592-598;608-614

Amidation site:

Amino acids 500-504

Cell attachment sequence:

Amino acids 149-152

Multicopper oxidases signature 1:

Amino acids 445-466

Immunoglobulin domain:

Amino acids 326-377

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FIGURE 585

GCCCGCCTGAGGAAGCCGTGTGCCTGGGATGCCAAGAGCCAGAGAATGGATCTTCTCCGAGTG
GGGACATTGCTGACAATCCCGGCTTCCCGAGGGCGGCTAAGAACAGGCAGTTTGTGTCTGGCTGG
CTGCAGATACCCAGAGGCACAAAGAGACCGAAGCCACCCGGAGGGACCCACGGACGGACAGAT
GGTAGGCGCGAACCCGAGAGGACCGGCGGAGGCTGAGCACCGAGAGCCGCCAAGGAAGAGAAA
CTAACCACAGCCAAGTTACCCCGCCGGCTTTCCCTTCGCTGCGCTAAGGAATGAAACCCTTCCA
GCTCGATCTGCTCTTTCGTCTGCTTCTTCCTCTTCAGTCAAGAGCTGGGCCTCCAGAAGAGAGG
ATGCTGTCTGGTGCTGGGCTACATGGCCAAGGACAAGTTTCGGAGAATGAATGAAGGCCAAGT
CTATTCCTTCAGCCAGCAGCCCCAGGACCAGGTGGTGGTGTCTGGGACAGCCAGTGACGCTACT
TTGCGCCATCCCCGAATACGATGGCTTCGTTCTGTGGATCAAGGACGGCTTGGCTCTGGGTGT
GGGCAGGGACCTCTCAAGTTACCCACAGTACCTGGTGGTAGGGAACCACTGTCAGGGGAGCA
CCACCTGAAGATCCTGAGGGCAGAGCTGCAAGACGATGCGGTGTACGAGTGCCAGGCCATCCA
GGCCGCCATCCGCTCCCGCCCCGCACGCCTCACAGTCCTGGTGCCGCCTGATGACCCCGTCAT
CCTGGGGGGCCCTGTGATCAGCCTGCGTGCGGGGGACCTCTCAACCTCACCTGCCACGCAGA
CAATGCCAAGCCTGCAGCCTCCATCATCTGGTTGCGAAAGGGAGAGGTCATCAATGGGGCCAC
CTACTCCAAGACCCTGCTTCGGGACGGCAAGCGGGAGAGCATCGTCAGCACCCCTCTTCATCTC
CCCTGGTGACGTGGAGAATGGCCAGAGCATCGTGTGTCTGTCGCCACCAACAAAGCCATCCCCGG
AGGAAAGGAGACGTGCGTCACCATTGACATCCAGCACCCCTCCACTGGTCAACCTCTCGGTGGA
GCCACAGCCAGTGCTGGAGGACAACGTCGTCACTTTCCACTGCTCTGCAAAGGCCAACCAGC
TGTCACCCAGTACAGGTGGGCCAAGCGGGGCCAGATCATCAAGGAGGCATCTGGAGAGGTGTA
CAGGACCACAGTGGACTACACGTACTTCTCAGAGCCCGTCTCCTGTGAGGTGACCAACGCCCTG
GGCAGCACCAACCTCAGCCGCACGGTTGACGTCTACTTTGGGCCCCGGATGACCACAGAACCC
CAATCCTTGCTCGTGGATCTGGGCTCTGATGCCATCTTCAGCTGCGCCTGGACCGGCAACCCA
TCCCTGACCATCGTCTGGATGAAGCGGGGCTCCGGAGTGGTCTGAGCAATGAGAAGACCCTG
ACCCTCAAATCCGTGCGCCAGGAGGACGCGGGCAAGTACGTGTGCCGGGCTGTGGTGCCCCGT
GTGGGAGCCGGGGAGAGAGAGGTGACCCTGACCGTCAATGGACCCCCCATCATCTCCAGCACC
CAGACCCAGCACGCCCTCCACGGCGAGAAGGGCCAGATCAAGTGCTTCATCCGGAGCACGCCG
CCGCCGGACCGCATCGCCTGGTCTGGAAGGAGAACGTTCTGGAGTCGGGCACATCGGGGCGC
TATACGGTGGAGACCATCAGCACCGAGGAGGGCGTCATCTCCACCCTGACCATCAGCAACATC
GTGCGGGCCGACTTCCAGACCATCTACAACCTGCACGGCCTGGAACAGCTTCGGCTCCGACACT
GAGATCATCCGGCTCAAGGAGCAAGGTTCTGGAAATGAAGTCGGGAGCCGGGCTGGAAGCAGAG
TCTGTGCCGATGGCCGTCATCATTGGGGTGGCCGTAGGAGCTGGTGTGGCCTTCCTCGTCCTT
ATGGCAACCATCGTGGCGTTCTGCTGTGCCCCGTTCCCAGAGAAGTACGGGAGGGAGATCCGGG
ATCTCAGGGAGGGGGACAGAGAAAAAGGCCAGGCTTAGGCTGCCCCGGAGAGCAAGTAAGCAG
GAGTGCAATGAACAGGGGTCCTAACAGTGCTGTGAGCTCCTGGGGCAGGGAGTGGGTCTGATG
CATCGGTGTATGTGAGCCTGGGCAACATGGCGCCTGGCAGAGTGGGCGCTAGGCTGAGGTTGA
CCTGGACTAGACTGAACTTCATCTGCAGGGCAGCCAGCATTTTGGATTGAACACATAGCTCTT
TCAGTCAGGAACTGTACAGAAAGATAGGGGGAAAAGCGGTTTGTGGTTTGATCCTTGCTCTAC
AAGAGCTGTTAGTCTAGAGAGACCCCATCTCTACAACAAAATAAAAATAAAGAGCTGCTAGTC
TCACCAGAAAAGCAGGTCACTCACACAGCTGTGGGGGAGTGGGTGGGGAAGCAATAAAGGAAT
TGCTTTGAGAAAACCTTAA

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FIGURE 586

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA148004
><subunit 1 of 1, 600 aa, 1 stop
><MW: 65308, pI: 8.35, NX(S/T): 5
MKPFQLDLLFVCFFLFSQELGLQKRGCCCLVLGYMAKDKFRRMNEGQVYSFSQQPQDQVVV
SGQPVTLLCAIPEYDGFVLWIKDGLALGVGRDLSSYPQYLVVGNHLSGEHHLKILRAELQ
DDAVYECQAIQAAIRSRPARLTVLVPPDDPVILGGPVISLRAGDPLNLTCHADNAKPAAS
IIWLRKGEVINGATYSKTLRLDGKRESIVSTLFI SPGDVENGQSIVCRATNKAI PGGKET
SVTIDIQHPPLVNLSVEPQPVL EDNVVTFHCSAKANPAVTQYRWAKRGQIIKEASGEVYR
TTVDYTYFSEPVSCVETNALGSTNLSRTVDVYFGPRMTTEPQSLLDLGSDAIFSCAWTG
NPSLTIVWMKRSGGVLSNEKTLTLKSVRQEDAGKYVCRAVVP RVGAGEREVTLT VNGPP
IISSTQTQHALHGEKGQIKCFIRSTPPPDRIAWSKENVLES GTSGRYTVETISTEEGVI
STLTISNIVRADFQTIYNCTAWNSFGSDTEIIRLKEQGSEMKSGAGLEAESVPM AVIIGV
AVGAGVAFLVLMATIVAFCCARSQRSTGGRSGISGRGTEKKARLRLPRRASKQECNEQGS

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 534-555

N-glycosylation sites:

Amino acids 167-171;253-257;324-328;498-502

Glycosaminoglycan attachment sites:

Amino acids 523-527;574-578

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 204-208;370-374;588-592

Tyrosine kinase phosphorylation sites:

Amino acids 40-49;300-308;389-397

N-myristoylation sites:Amino acids 45-51;62-68;84-90;103-109;192-198;236-242;
374-380;436-442;478-484;539-545;543-549;
568-574**Amidation site:**

Amino acids 202-206

Leucine zipper pattern:

Amino acids 8-30

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FIGURE 587

CAAAAAAGGAGCATGTCTTCATCCATGAGAGGCCTCGAAAAATCAATGGTATTTGCATTTCTC
CCAAGAAGGTTGCTTGCCAAAACCTTTTCGGCCATTTTCTGCTTTCAGAGTGAGACAAAGTTCA
AAATGACAGTCTGTCAGCTCATTGAAGGCACTAGATACCCTGCCTGCAGGTACCACTATTCCC
CCACAGAGGGGTTTGTCTTGTCACTTGTGATGACTTGAGGCCAGATAGTTTCCTTGGCTATG
TTAAATAACTCAAGATCAGCTACCGAGTCTGAGATCTCTTCTCTCATGGCATTGGAGCTGGCT
GTGCCTGAGGCAGACCTGGACCGTGGACATGGGGCAATGCCTTGAGCGGAAGGGGAAGCCACT
GAATTTTGGGTGTCACCAGGTAAACAGAGCCCTCAGCATCTGAATAGAACTGAACAGGAACA
GAAGAGATTACACTACATCTGAGATGGAGACCTTTCCTCTGCTGCTGCTCAGCCTGGGCCTGG
TTCTTGCAGAAGCATCAGAAAGCACAAATGAAGATAATTAAAGAAGAATTTACAGACGAAGAGA
TGCAATATGACATGGCAAAAAGTGGCCAAGAAAAACAGACCATTGAGATATTAATGAACCCGA
TCCTGTTAGTTAAAAATACCAGCCTCAGCATGTCCAAGGATGATATGTCTTCCACATTACTGA
CATTCAGAAGTTTACATTATAATGACCCCAAGGGAAACAGTTCGGGTAATGACAAAGAGTGTT
GCAATGACATGACAGTCTGGAGAAAAGTTTCAGAAGCAAACGGATCGTGCAAGTGGAGCAATA
ACTTCATCCGCAGCTCCACAGAAGTGATGCGCAGGGTCCACAGGGCCCCCAGCTGCAAGTTTGTA
CAGAATCCTGGCATAAGCTGCTGTGAGAGCCTAGAACTGGAAAATACAGTGTGCCAGTTCCTACT
ACAGGCAAACAATTCCCCAGGTGCCAATAACCATAGTGTTACCTCATTAGAGAAGATATTGACA
GTGCTGACAGGTCATTCTCTGATGAGCTGGTTAGTTTGTGGCTCTAAGTTGTAAATCCCACAG
AGCTTTAGGACTAGGGTCTTACTAAAGAAGGACCTCTTCTTGTTCAATTCTTGTTTAAACCTTT
CCTTAATATCTACTCTTTAGCACTATAGTGAACCTGATTATTTATTCTAACTGGAGGAGTG
AAAAATCCAAAATTGTGGATAATTCAATTAAAAGTTATGACTGATACCG

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FIGURE 588

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149893
><subunit 1 of 1, 199 aa, 1 stop
><MW: 22427, pI: 6.46, NX(S/T): 3
METFPLLLLSLGLVLAEASESTMKIIEEFTDEEMQYDMAKSGQEKQTIEILMNPILLVK
NTSLSMSKDDMSSTLLTFRSLHYNDPKGNSGNDKECCNDMTVWRKVSEANGSCKWSNNE
IRSSTEVMRRVHRAPSCKFVQNPGISCCESLELENTVCQFTTGKQFPRCQYHSVTSLEKI
LTVLTGHSLMSWLVCESKL

Important features of the protein:**Signal peptide:**

Amino acids 1-16

N-glycosylation sites:

Amino acids 61-65;89-93;111-115

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 105-109

N-myristoylation sites:

Amino acids 12-18;88-94;144-150

Microbodies C-terminal targeting signal:

Amino acids 197-201

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FIGURE 589

CAGTCCTGCCGGGACGGTGAGCGCATTTCAGCACCCCTGGACAGCACCGCGGTTGCGCTGCCTCC
AGGGCGGCCCCGGGCTGCTCCTGCTCCGCAGAGCTACGCCCTCCCCCGGGTGCCCCGGACCC
TGCACTTGCCGCCGCTTTCCTCGCGCTGCTCTGGACCTTGCTAGCCGGCTCTGCACCTCCCAG
AAGCCGTGGGCGCGCCGCTCAGCTGCTCCATCGCCTCACTTTCCCAGGCTCGCGCCCGAAGCA
GAGCCATGAGAACCCAGGGTGCCCTGGCGAGCCGCTAGCGCCATGGGGCCCCGGCGAGGCGCTG
CTGGCGGGTCTCCTGGTGATGGTACTGGCCGTGGCGCTGCTATCCAACGCACTGGTGCTGCTT
TGTTGCGCCTACAGCGCTGAGCTCCGCACTCGAGCCTCAGGCGTCCTCCTGGTGAATCTGTCT
CTGGGCCACCTGCTGCTGGCGGCGCTGGACATGCCCTTCACGCTGCTCGGTGTGATGCGCGGG
CGGACACCGTCGGCGCCCGGCGCATGCCAAGTCATTGGCTTCCTGGACACCTTCCTGGCGTCC
AACGCGGCGCTGAGCGTGGCGGCGCTGAGCGCAGACCAGTGGCTGGCAGTGGGCTTCCCCTG
CGCTACGCCGGACGCCTGCGACCGCGCTATGCCGGCCTGCTGCTGGGCTGTGCCTGGGGACAG
TCGCTGGCCTTCTCAGGCGCTGCACTTGGCTGCTCGTGGCTTGGCTACAGCAGCGCCTTCGCG
TCCTGTTGCTGCGCCTGCCGCCCGAGCCTGAGCGTCCGCGCTTCGCAGCCTTCACCGCCACG
CTCCATGCCGTGGGCTTCGTGCTGCCGCTGGCGGTGCTCTGCCTCACCTCGCTCCAGGTGCAC
CGGGTGGCACGCAGACACTGCCAGCGCATGGACACCGTCACCATGAAGGCGCTCGCGCTGCTC
GCCGACCTGCACCCCACTGTGCGGCAGCGCTGCCTCATCCAGCAGAAGCGGCGCCGCCACCGC
GCCACCAGGAAGATTGGCATTGCTATTGCGACCTTCCTCATCTGCTTTGCCCCGTATGTCATG
ACCAGGCTGGCGGAGCTCGTGCCCTTCGTACCGTGAACGCCCACTGGGGCATCCTCAGCAAG
TGCCTGACCTACAGCAAGGCGGTGGCCGACCCGTTACGTACTCTCTGCTCCGCCGGCCGTTT
CGCCAAGTCCTGGCCGGCATGGTGACCGGCTGCTGAAGAGAACCCCGCGCCCAGCATCCACC
CATGACAGCTCTCTGGATGTGGCCGGCATGGTGACACAGCTGCTGAAGAGAACCCCGCGCCCA
GCGTCCACCCACAACGGCTCTGTGGACACAGAGAATGATTCTGCTGCTGACGACACACTGA
GGGCTGGCAGGGCTCATCGCCCCACCTTCTAAGAAGCCCTGTGGAAAGGGCACTGGCCCTG
CCACAGAGATGCCACTGGGGACCCCGAGACACCAGTGGCTTGACTTTGAGCTAAGGCTGAG

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FIGURE 590

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149930
><subunit 1 of 1, 363 aa, 1 stop
><MW: 39332, pI: 10.42, NX(S/T): 3
MGPGEALLAGLLVMVLAVALLSNALVLLCCAYSaelRTRASGVLLVNLSLGHLLLAALDM
PFTLLGVMRGRTPSAPGACQVIGFLDTFLASNAALSVAALSADQWLAVGFPLRYAGRLRP
RYAGLLLGCAWGQSLAFSGAALGCSWLGYSSAFASCSLRLPPEPERPRFAAFTATLHAVG
FVLPLAVLCLTSLQVHRVARRHCRMDTVTMKALALLADLHPSVRQRCLIQOKRRRHRAT
RKIGIAIATFLICFAPYVMTRLAELVPFVTVNAQWGILSKCLTYSKAVADPFTYSLLRP
FRQVLAGMVHRLKRTPRPASTHDSSLDVAGMVHQLLKRTPRPASTHNGSVDTENDSCLQ
QTH
```

Important features of the protein:**Signal peptide:**

Amino acids 1-24

Transmembrane domains:

Amino acids 46-60;85-103;130-150;175-192;246-264

N-glycosylation sites:

Amino acids 47-51;348-352;355-359

Tyrosine kinase phosphorylation site:

Amino acids 286-295

N-myristoylation sites:Amino acids 66-72;124-130;128-134;132-138;139-145;244-250;
349-355**G-protein coupled receptor proteins:**

Amino acids 72-112

7 transmembrane receptor (rhodopsin family):

Amino acids 22-294

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FIGURE 591

AACATGGCTGCGGCGCCTGGGCTGCTCGTCTGGCTGCTCGTGCTCCGGCTGCCCTGGCGGGTG
CCGGGCCAGCTGGACCCCAGCACTGGCCGGCGGTTCTCGGAGCACAACTCTGCGCGGACGAC
GAATGCAGCATGATGTACCGCGGTGAGGCTCTTGAAGATTTACAGGCCCGGATTGTCGTTTT
GTGAATTTTAAAAAAGGTGATCCTGTATATGTTTACTATAAACTGGCAAGAGGATGGCCTGAA
GTTTGGGCTGGAAGTGTTGGACGCACCTTTTGGATATTTTCCAAAAGATTTAATCCAGGTAGTT
CATGAATATACCAAAGAAGAGCTACAAGTTCCAACAGATGAGACGGATTTTGTGTTGTTTGTAT
GGAGGAAGAGATGATTTTTCATAATTATAATGTAGAAGAACTTTTAGGGTTTTTGGAACTGTAC
AATTCTGCAGCTACAGATTCTGAGAAAGCTGTAGAAAAAACTTTACAGGATATGGAAAAAAC
CCTGAATTATCTAAGGAAAGGGAACCTGAACCTGAACCAGTAGAAGCCAACCTCAGAGGAAAGT
GATAGTGTATTCTCAGAAAACACTGAGGATCTTCAGGAACAGTTTACAACCTCAGAAGCACCAC
TCCCATGCAAACAGCCAAGCAAATCATGCTCAGGGAGAGCAGGCTTCATTTGAATCTTTTGAA
GAAATGCTGCAAGATAAACTAAAAGTGCCAGAAAGTGAAAACAACAAAACCAGCAATAGTTCT
CAGGTCTCAAATGAACAGGATAAGATTGATGCCTATAAACTTTTGAAAAAAGAAATGACTCTA
GACTTGAAAACCAAATTTGGCTCAACAGCTGATGCACTTGTATCTGATGATGAGACAACCAGA
CTCGTTACTTCATTAGAAGATGATTTTGATGAGGAATTGGATACTGAGTATTATGCAGTTGGA
AAGGAAGATGAGGAGAACCAAGAAGACTTTGATGAGTTGCCATTACTTACCTTTACAGATGGG
GAAGATATGAAAACCTCCAGCAAAGTCTGGCGTTGAGAAATATCCAACAGATAAAGAGCAGAAT
TCAAATGAAGAGGACAAGGTTCACTAACTGTGCCCCCTGGCATCAAAAATGATGATAAAAAT
ATACTAACAACTGGGGGGGACACTATCTTCTCTATTGTACAGGAGGTGAAGAAACAAGAGAT
ACGATGGATTTAGAGAGCTCTAGTTCAGAGGAAGAAAAAGAAGATGATGATGATGCATTAGTC
CCAGATAGCAAACAGGGGAAACCACAGTCAGCAACAGATTATAGTGACCCTGACAATGTAGAT
GATGGTCTTTTTTATTGTAGACATTCCTAAAACAAATAATGACAAAGAAGTAAACGCAGAACAT
CACATTAAAGGAAAAGGGAGGGGAGTTCAAGGAATCCAAGAGGGGCCCTGGTACAAGATGAGACA
GAATTAGAGGATGAAAATCAAGAAGGCTTTAAACAGAGCCCATAAAACTATGACCTCTGAGG
TTTCATTGGAAAGAAAGTGTAAGTGTGCAATTATCCATTACAGTAAAGGATTTTCATTGGCTTCAA
AATCCAAAAGTTTATTTTAAAAGGTTTGTGTTAGAACTAAGCTGCCTTGGCAGTGTGCATTT
TTGAGCCAAACAATTCAAAAATGTCATTTCTTCCCTAAATAAAAATCACCTTTTAAGCTAGAG
CGTCCTTACAACCTTTGAAATGTGCAATAAAGAATACCTGTGTTTTAGCTAATGTAGCATATGT
AATTGCAAAATGATTTAGAATGTCATGAAAAATATGAACATTTCCCTGTGGAAATGCTTTAAGA
ACATGTATTTCCATTATCCTATTTTTTAGTGTACACCAGCTGAATACGGAGCAATGGTGTGTTAT
AAGCGTTTTTTTAACTATCTGGTCACAAAGACTGTTACGCTAAAAATGTTTACTAAAAGATC
ACTAACTATCTCCCCTCTTGCTGAAGTTCTTTGTAGTAATAGCTCATAAAAATTTGTTTATT
AATATTTAAAAA

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FIGURE 592

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150157
><subunit 1 of 1, 499 aa, 1 stop
><MW: 56471, pI: 4.31, NX(S/T): 2
MAAAPGLLVWLLVLRLLPWRVPGQLDPSTGRRFSEHKLCADDECSMMYRGEALEDFTGPDC
RFVNFKKGDPVYVYYKLARGWPEVWAGSVGRFTGYFPKDLIQVVHEYTKHEELQVPTDET
FVCFDGGRRDDFHNYNVEELLGFLELYNSAATDSEKAVEKTLQDMEKNPELSKEREPEPEP
VEANSEESDSVFSSENTEDLQEQFTTQKHHSANSQANHAQGEQASFESFEEMLQDKLKVP
ESENKTSNSSQVSNEQDKIDAYKLLKKEMTLDLKTKFGSTADALVSDDETTRLVTSLED
DFDEELDTEYYAVGKEDEENQEDFDELPLLTFTDGEDMKTPAKSGVEKYPTDKEQNSNEE
DKVQLTVPPGIKNDDKNILTTWGDITFSIVTGGEETRDMDLESSSSEEEKEDDDDALVP
DSKQKGKQSATDYSDDPNVDDGLFIVDIPKTNNDKEVNAAEHKKGKGRGVQESKRGLVQD
ETELEDENQEGFKTEPIKL

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-glycosylation sites:

Amino acids 245-249;249-253

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 30-34

Tyrosine kinase phosphorylation site:

Amino acids 66-72

N-myristoylation sites:

Amino acids 392-398;469-475

Amidation site:

Amino acids 28-32

Aminoacyl-transfer RNA synthetases class-II signature 1:

Amino acids 47-70

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FIGURE 593

GGGCCAGTAGAGTGTGTCTGGGTCAGCTGAGTGACTACATCAAAGCTCCCAGCCTTGAAAAAC
ACATGCTGTTCCCAGGCCTCAAGATATTGAAACATTAATTAGATAATTTAAAGTAGCGTTTTTC
TTCTACAATGTCTGAAGAAGTGACCTACGCGACACTCACATTTTCAGGATTCTGCTGGAGCAAG
GAATAACCGAGATGGAAATAACCTAAGAAAAAGAGGGCATCCAGCTCCATCTCCCATTGCGG
TCATGCTGCTCTGGGTCTGGTAACTCTTTGCCTGATGTTGCTGATTGGGCTGGTGACGTTGGG
GATGATGTTTTTGCAGATATCTAATGACATTAACCTCAGATTCAGAGAAATTGAGTCAACTTCA
GAAAACCATCCAACAGCAGCAGGATAACTTATCCCAGCAACTGGGCAACTCCAACAACCTTGTC
CATGGAGGAGGAATTTCTCAAGTCACAGATCTCCAGTCTACTGAAGAGGCAGGAACAAATGGC
CATCAAACCTGTGCCAAGAGCTAATCATTCACTTTCAGACCACAGATGTAATCCATGTCCTAA
GATGTGGCAATGGTACCAAAATAGTTGCTACTATTTTACAACAAATGAGGAGAAAACCTGGGC
TAACAGTAGAAAGGACTGCATAGACAAGAACTCCACCCTAGTGAAGATAGACAGTTTGGAAGA
AAAGGATTTTCTTATGTCACAGCCATTACTCATGTTTTTCGTTCTTTTGGCTGGGATTATCATG
GGACTCCTCTGGCAGAAGTTGGTTCTGGGAAGATGGCTCTGTTCCCTCTCCATCCTTGTACGT
CTCTAACTATTGAGGGTAAACACAAGCTTTCCATGGAATCCTGGGAAAATTAATAATGATTGT
GAGAATTATAAATACAGACATAAAAAGAGGAGTACAACATACTGAGAAAAGAGCTCCAGTAAC
AAATATTGAAAGGAGATTTAGTACTAAAGAACTTGACCAGATCAATGGATCCAAAGGATGTGC
TTATTTTCAAAAAGGAAATATTTATATTTCTCGCTGTAGTGCTGAAATTTTTTGGATTGCGA
GAAGACAGCTGCCCCAGTGAAGACTGAGGATTTGGATTAGTATGCTTCTTCCAAATTCTCCAA
GAAGTAAGAGACTTGTGAGTAAGCTCATATGAGGAAAGAGGAACTACGGTACCAGAGCAAGG
CGGAATTCTGCA

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FIGURE 594

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA150163
><subunit 1 of 1, 232 aa, 1 stop
><MW: 26754; pI: 5.80; NX(S/T): 3
MSEEVTYATLTFQDSAGARNNRDGNLRLKRGHPAPSPIWRHAALGLVTLCIMLLIGLVTL
GMMFLQISNDINSDEKLSQLQKTIQQQQDNLSQQLGNSNNLSMEEEFLLKSQISSLLKRQ
EQMAIKLCQELIHTSDHRCNCPKMWQWYQNSCYFFTTNEEKTWANSRKDCIDKNSTLV
KIDSLEEKDFLMSQPLLMFSFFWLGLSWDSSGRSWFWEDGSVPSPSLYVSNY
```

Important features of the protein:**Transmembrane domain:**

Amino acids 42-62

N-glycosylation sites:

Amino acids 91-95;101-105;176-180

N-myristoylation sites:

Amino acids 17-23;97-103

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FIGURE 595

CGGACGCGTGGGGAAGAGGAGGAGGAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAG
AACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAGGGAGAGGAAAAGAGAGCCTAGGAGAACC
ATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCTTCTTGCCCTATGCTGACA
GCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATAACAACACT
GTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATG
GATGAACATAATAGGCCCATTCACACATAACCAGGTATGTAATGTAATGGAACCAAACCAAAAC
AACTGGCTTCGTACAAACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAA
TTCACACTAAGGGATTGTAACAGCATCCCATGGGTCTTGGGGACTTGCAAAGAAACATTTAAT
CTGTTTTATATGGAATCAGATGAGTCCACGGAATTAAATTCAAGCCAAACCAGTATACAAAG
ATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTGATCGCATCCTCAA
CTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTTCAA
GACATTGGGGCGTGCAATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCTTCACT
GTTTCGTAACCTTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCCTCCTCTTTGGTTGAA
GTACGGGGTTCTTGTGTGAAGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCT
GATGGAGATTGGCTGGTTCCTCTTGGAAGGTGCATCTGCAGTACAGGATATGAAGAAATTGAG
GGTTCTTGCCATGGAGCCTCCAAAGGCCGCTGCTTCTTAGTTGGCCATCTTGGCCCCACCCCGA
AACAGTAACCTTTGAAGAATAAAAGAAAAAGCAAAAGAGTAGCATTACTAAAATATTAAACGG
TTACATTTACAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 596

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA153579
><subunit 1 of 1, 285 aa, 1 stop
><MW: 32368, pI: 5.32, NX(S/T): 0
MGGCEVREFLLQFGFFLPMLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAQFDIGACIALVSVRVFYKKCPFTVRNLMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPPLGRCICSTGYEEIEGSCHGASKGRCE

Important features of the protein:**Signal peptide:**

Amino acids 1-22

N-myristoylation sites:

Amino acids 192-198;274-280;278-284

Receptor tyrosine kinase class V signature 1:

Amino acids 192-209

Ephrin receptor ligand binding domain:

Amino acids 34-207

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FIGURE 597

ACACTGGCCAAACAAAAACGAAAGCACTCCGTGCTGGAAGTAGGAGGAGAGTCAGGACTCCCA
GGACAGAGAGTGCACAACTACCCAGCACAGCCCCCTCCGCCCCCTCTGGAGGCTGAAGAGGG
ATTCCAGCCCCCTGCCACCCACAGACACGGGCTGACTGGGGTGTCTGCCCCCCTTGGGGGGGGG
CAGCACAGGGCCTCAGGCCTGGGTGCCACCTGGCACCTAGAAG**ATG**CCTGTGCCCTGGTTCTT
GCTGTCCTTGGCACTGGGCCGAAGCCCAGTGGTCCTTTCTCTGGAGAGGCTTGTGGGGCCTCA
GGACGCTACCCACTGCTCTCCGGGCCTCTCCTGCCGCCTCTGGGACAGTGACATACTCTGCCT
GCCTGGGGACATCGTGCTGCTCCGGGGCCCCGTGCTGGCGCCTACGCACCTGCAGACAGAGCT
GGTGCTGAGGTGCCAGAAGGAGACCGACTGTGACCTCTGTCTGCGTGTGGCTGTCCACTTGGC
CGTGCAATGGGCACTGGGAAGAGCCTGAAGATGAGGAAAAGTTTGGAGGAGCAGCTGACTCAGG
GGTGGAGGAGCCTAGGAATGCCTCTCTCCAGGCCCAAGTCGTGCTCTCCTTCCAGGCCTACCC
TACTGCCCCGCTGCGTCCTGCTGGAGGTGCAAGTGCCTGCTGCCCTTGTGCAGTTTGGTCAGTC
TGTGGGCTCTGTGGTATATGACTGCTTCGAGGCTGCCCTAGGGAGTGAGGTACGAATCTGGTC
CTATACTCAGCCCAGGTACGAGAAGGAACTCAACCACACACAGCAGCTGCCTGCCCTGCCCTG
GCTCAACGTGTGAGCAGATGGTGACAACGTGCATCTGGTTCTGAATGTCTCTGAGGAGCAGCA
CTTCGGCCTCTCCCTGTACTGGAATCAGGTCCAGGGCCCCCCCCAAAACCCCGGTGGCACAAAAA
CCTGACTGGACCGCAGATCATTACCTTGAACCACACAGACCTGGTTCCCTGCCCTCTGTATTCA
GGTGTGGCCTCTGGAACCTGACTCCGTTAGGACGAACATCTGCCCCCTTCAGGGAGGACCCCCG
CGCACACCAGAACCTCTGGCAAGCCGCCCGACTGCGACTGCTGACCCTGCAGAGCTGGCTGCT
GGACGCACCGTGCTCGCTGCCCGCAGAAGCGGCACTGTGCTGGCGGGCTCCGGGTGGGGACCC
CTGCCAGCCACTGGTCCCACCGCTTTTCTGGGAGAACGTCACTGTGGACAAGGTTCTCGAGTT
CCCATTGCTGAAAGGCCACCCTAACCTCTGTGTTTCAAGTGAACAGCTCGGAGAAGCTGCAGCT
GCAGGAGTGCTTGTGGGCTGACTCCCTGGGGCCTCTCAAAGACGATGTGCTACTGTTGGAGAC
ACGAGGCCCCCAGGACAACAGATCCCTCTGTGCCTTGAACCCAGTGGCTGTACTTCACTACC
CAGCAAAGCCTCCACGAGGGCAGCTCGCCTTGGAGAGTACTTACTACAAGACCTGCAGTCAGG
CCAGTGTCTGCAGCTATGGGACGATGACTTGGGAGCGCTATGGGCCTGCCCCATGGACAAATA
CATCCACAAGCGCTGGGCCCTCGTGTGGCTGGCCTGCCTACTCTTTGCCGCTGCGCTTTCCCT
CATCCTCCTTCTCAAAAAGGATCACGCGAAAGGGTGGCTGAGGCTCTTGAAACAGGACGTCCG
CTCGGGGGCGGGCCGAGGGGCGCGCGGCTCTGCTCCTCTACTCAGCCGATGACTCGGGTTT
CGAGCGCCTGGTGGGCGCCCTGGCGTCGGCCCTGTGCCAGCTGCCGCTGCGCGTGGCCGTAGA
CCTGTGGAGCCGTGCTGAACTGAGCGCGCAGGGGCCCCGTGGCTTGGTTTCACGCGCAGCGGCG
CCAGACCCTGCAGGAGGGCGGCGTGGTGGTCTTGTCTTCTCTCCCGGTGCGGTGGCGCTGTG
CAGCGAGTGGCTACAGGATGGGGTGTCCGGGCCCCGGGGCGCACGGCCCCGCACGACGCCTTCCG
CGCCTCGCTCAGCTGCGTGCTGCCCGACTTCTTGCAGGGGCCGGGCGCCCCGGCAGCTACGTGGG
GGCCTGCTTCGACAGGCTGCTCCACCCGGACGCCGTACCCGCCCTTTTCCGCACCGTGCCCGT
CTTCACACTGCCCTCCCAACTGCCAGACTTCCTGGGGGCCCTGCAGCAGCCTCGCGCCCCGCG
TTCCGGGCGGCTCCAAGAGAGAGCGGAGCAAGTGTCCCGGGCCCTTCAGCCAGCCCTGGATAG
CTACTTCCATCCCCCGGGGACTCCCGCGCCGGGACGCGGGGTGGGACCAGGGGCGGGACCTGG
GGCGGGGGACGGGACT**TAA**AATAAAGGCAGACGCTGTTTTTCTAAAAAA

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FIGURE 598

```
></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA164625
><subunit 1 of 1, 705 aa, 1 stop
/><MW: 76970, pI: 6.00, NX(S/T): 9
MPVPWFLLSLALGRSPVVLSELRVGPQDATHCSPGLSCRLWDS DILCLPGDIVPAPGP
VLAPTHLQTELVLRQCKETDCDLCLRVAVHLAVHGHWEPEDEEKFGGAADSGVEEPRN
ASLQAQVVLSFQAYPTARCVLLEVQVPAALVQFGQSVGSSVYDCFEAALGSEVRIWSYT
QPRYEKELNHTQQLPALPWLNV SADGDNVHLVLNVSEEQHFGLSLYWNQVQGPPKPRWH
KNLTGPQIITLNHTDLVPCLCIQVWPLEPDSVRTNICPFREDPRAHQNLWQAARLRLLT
LQSWLLDAPCSLPAAEALCW RAPGGDPCQPLVPPLSWENVTVDKVLEFP LLKGHPNLCV
QVNSSEKLQLQECLWADSLG PLKDDVLLLETRGPQDNRS LCALEPSGCTSLPSKASTRA
ARLGEYLLQDLQSGQCLQLW DDDL GALWACPMDKYIHKRWALVWLACLLFAAALSLILL
LKKDHAKGWLRLLLKQDV RSGAAARGRAALLLYSADDSGFERLVGALASALCQLPLRVAV
DLWSRRELSAQGPVAFWFAHQRRQTLQEGGVVLLFSPGAVALCSEWLQDGVSGPGAHPG
HDAFRASLSCVLPDFLQGRAPGSYVGACFDRL LHPDAVPALFRTVPVFTLPSQLPDFLG
ALQQPRAPRSGRLQERAEQVSRALQPALDSYFHPPGTPAPGRGVGPGAGPGAGDGT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-20

Transmembrane domain:

Amino acids 453-473

N-glycosylation sites:Amino acids 118-122;186-190;198-202;211-215;238-242;
248-252;334-338;357-360;391-395;**Glycosaminoglycan attachment site:**

Amino acids 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site:

Amino acids 552-556

N-myristoylation sites:Amino acids 107-113;152-158;319-325;438-444;516-522;612-618;
692-698;696-702;700-706

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FIGURE 599

GGTCCTTA**ATG**GCAGCAGCCGCCGCTACCAAGATCCTTCTGTGCCTCCCGCTTCTGCTCCTGC
TGTCCGGCTGGTCCCGGGCTGGGCGAGCCGACCCCTCACTCTCTTTGCTATGACATCACCGTCA
TCCCTAAGTTCAGACCTGGACCACGGTGGTGTGCGGTTCAAGGCCAGGTGGATGAAAAGACTT
TTCTTCACTATGACTGTGGCAACAAGACAGTCACACCTGTCAGTCCCCTGGGGAAGAACTAA
ATGTCACAACGGCCTGGAAAGCACAGAACCCAGTACTGAGAGAGGTGGTGGACATACTTACAG
AGCAACTGCGTGACATTCAGCTGGAGAATTACACACCCAAGGAACCCCTCACCTGCGAGGCAA
GGATGTCTTGTGAGCAGAAAGCTGAAGGACACAGCAGTGGATCTTGGCAGTTCAGTTTCGATG
GGCAGATCTTCCTCCTCTTTGACTCAGAGAAGAGAATGTGGACAACGGTTCATCCTGGAGCCA
GAAAGATGAAAGAAAAGTGGGAGAATGACAAGGTTGTGGCCATGTCCTTCCATTACTTCTCAA
TGGGAGACTGTATAGGATGGCTTGAGGACTTCTTGATGGGCATGGACAGCACCCCTGGAGCCAA
GTGCAGGAGCACCACTCGCCATGTCCTCAGGCACAACCCAACCTCAGGGCCACAGCCACCACCC
TCATCCTTTGCTGCCTCCTCATCATCCTCCCCTGCTTCATCCTCCCTGGCATC**TG**AGGAGAGT
CCTTTAGAGTGACAGGTTAAAGCTGATACCAAAGGCTCCTGTGAGCACGGTCTTGATCAAAC
TCGCCCTTCTGTCTGGCCAGCTGCCCACGACCTACGGTGTATGTCCAGTGGCCTCCAGCAGAT
CATGATGACATCATGGACCCAATAGCTCATTCAGTGCCTTGATTCCCTTTTGCCAACAATTTTA
CCAGCAGTTATACCTAACATATTATGCAATTTTCTCTTGGTGCTACCTGATGGAATTCCTGCA
CTTAAAGTTCTGGCTGACTAAACAAGATATATCATTTTCTTTCTTCTTTTTTGTGGAAAA
TCAAGTACTTCTTTGAATGATGATCTCTTTCTTGCAAATGATATTGTCAGTAAAATAATCACG
TTAGACTTCAGACCTCTGGGGATTCTTTCCGTGTCCTGAAAGAGAATTTTAAATTATTTAAT
AAGAAAAAATTTATATTAATGATTGTTTCCTTTAGTAATTTATTGTTCTGTACTGATATTTAA
ATAAAGAGTTCTATTTCCCAAAAAAAAAAAAAAAAAAAAA

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FIGURE 600

MAAAAATKILLCLPLLLLLSGWSRAGRADPHSLCYDITVIPKFRPGPRWCAVQGQVDEKTFH
YDCGNKTVTPVSP LGKKLNVT TAWKAQNPVLREVVDILTEQLRDIQLENYTPKEPLTLQARMS
CEQKAEGHSSGSWQFSFDGQIFLLFDSEKRMWTTVHPGARKMKEKWENDKVVAMSFHYFSMGD
CIGWLEDFLMGMDSTLEPSAGAPLAMSSGTTQLRATATTLILCCLLIILPCFILPGI

Important features:**Signal peptide:**

amino acids 1-25

Transmembrane domain:

amino acids 224-246

N-glycosylation site.

amino acids 68-72, 82-86

N-myristoylation site.

amino acids 200-206, 210-216

Amidation site.

amino acids 77-81

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FIGURE 601

GCAGTCAGAGACTTCCCCTGCCCCCTCGCTGGGAAAGAACATTAGGAATGCCTTTTAGTGCCTT
GCTTCCTGAACTAGCTCACAGTAGCCCGGCGGGCCCAGGGCAATCCGACCACATTTCACTCTCA
CCGCTGTAGGAATCCAGATGCAGGCCAAGTACAGCAGCACGAGGGACATGCTGGATGATGATG
GGGACACCACCATGAGCCTGCATTCTCAAGCCTCTGCCACAACCTCGGCATCCAGAGCCCCGGC
GCACAGAGCACAGGGCTCCCTCTTCAACGTGGCGACCAGTGGCCCTGACCCTGCTGACTTTGT
GCTTGGTGCTGCTGATAGGGCTGGCAGCCCTGGGGCTTTTGTTTTTTTCAGTACTACCAGCTCT
CCAATACTGGTCAAGACACCATTTCTCAAATGGAAGAAAGATTAGGAAATACGTCCCAAGAGT
TGCAATCTCTTCAAGTCCAGAATATAAAGCTTGACAGGAAGTCTGCAGCATGTGGCTGAAAAAC
TCTGTCGTGAGCTGTATAACAAAGCTGGAGCACACAGGTGCAGCCCTTGTACAGAACAATGGA
AATGGCATGGAGACAATTGCTACCAGTTCTATAAAGACAGCAAAAGTTGGGAGGACTGTAAAT
ATTTCTGCCTTAGTGAAAACCTACCATGCTGAAGATAAACAAACAAGAAGACCTGGAATTTG
CCGCGTCTCAGAGCTACTCTGAGTTTTTCTACTCTTATTGGACAGGGCTTTTGCGCCCTGACA
GTGGCAAGGCCTGGCTGTGGATGGATGGAACCCCTTTCACCTTCTGAACTGTTCCATATTATAA
TAGATGTCACCAGCCCCAAGAAGCAGAGACTGTGTGGCCATCCTCAATGGGATGATCTTCTCAA
AGGACTGCAAAGAATTGAAGCGTTGTGTCTGTGAGAGAAGGGCAGGAATGGTGAAGCCAGAGA
GCCTCCATGTCCCCCTGAAACATTAGGCGAAGGTGACTGATTCGCCCTCTGCAACTACAAAT
AGCAGAGTGAGCCAGGCGGTGCCAAAGCAAGGGCTAGTTGAGACATTGGGAAATGGAACATAA
TCAGGAAAGACTATCTCTCTGACTAGTACAAAATGGGTTCTCGTGTTTCCTGTTTCAGGATCAC
CAGCATTCTGAGCTTGGGTTTATGCACGTATTTAACAGTCACAAGAAGTCTTATTTACATGC
CACCAACCAACCTCAGAAACCCATAATGTCATCTGCCTTCTTGGCTTAGAGATAACTTTTAGC
TCTCTTTCTTCTCAATGTCTAATATCACCTCCCTGTTTTTCATGTCTTCCTTACACTTGGTGGA
ATAAGAAACTTTTTGAAGTAGAGGAAATACATTGAGGTAACATCCTTTTCTCTGACAGTCAAG
TAGTCCATCAGAAATTGGCAGTCACTTCCCAGATTGTACCAGCAAATACACAAGGAATTCTTT
TTGTTTGTTTCAGTTCATACTAGTCCCTTCCCAATCCATCAGTAAAGACCCCATCTGCCTTGT
CCATGCCGTTTCCCAACAGGGATGTCACCTGATATGAGAATCTCAAATCTCAATGCCTTATAA
GCATTCCCTCCTGTGTCCATTAAGACTCTGATAATTGTCTCCCCTCCATAGGAATTTCTCCCA
GGAAAGAAATATATCCCCATCTCCGTTTCATATCAGAACTACCGTCCCCGATATTCCCTTCAG
AGAGATTAAAGACCAGAAAAAAGTGAGCCTCTTCATCTGCACCTGTAATAGTTTCAGTTCCTA
TTTTCTTCCATTGACCCATATTTATACCTTTCAGGTACTGAAGATTTAATAATAATAAATGTA
AATACTGTGAAAAA

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FIGURE 602

MQAKYSSTRDMLDDDGD TTMSLHSQASATTRHPEPRRTEHRAPSSTWRPVALTLLTLCIVLLI
GLAALGLLFFQYYQLSNTGQDTISQMEERLGNTSQELQSLQVQNIKLAGSLQHVAEKLCRELY
NKAGAHRCSPCTEQWKWHGDNCYQFYKDSKSWEDCKYFCLSENSTMLKINKQEDLEFAASQSY
SEFFYSYWTGLLRPDSGKAWLWMDGTPFTSELFHIIIDVTSPRSRDCVAILNGMIFSKDCKEL
KRCVCERRAGMVKPESLHVPPETLGEGD

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FIGURE 603

GGGAGAGAGGATAAATAGCAGCGTGGCTTCCCTGGCTCCTCTCTGCATCCTTCCCGACCTTCC
CAGCAATATGCATCTTGCACGTCTGGTGGCTCCTGCTCCCTCCTTCTGCTACTGGGGGCCCT
GTCTGGATGGGCGGCCAGCGATGACCCCATTTGAGAAGGTCATTGAAGGGATCAACCGAGGGCT
GAGCAATGCAGAGAGAGAGGTGGGCAAGGCCCTGGATGGCATCAACAGTGGAATCACGCATGC
CGGAAGGGAAGTGGAGAAGGTTTTCAACGGACTTAGCAACATGGGGAGCCACACCGGCAAGGA
GTTGGACAAAGGCGTCCAGGGGCTCAACCACGGCATGGACAAGGTTGCCCATGAGATCAACCA
TGGTATTGGACAAGCAGGAAAGGAAGCAGAGAAGCTTGGCCATGGGGTCAACAACGCTGCTGG
ACAGGCCGGGAAGGAAGCAGACAAAGCGGTCCAAGGGTTCCACACTGGGGTCCACCAGGCTGG
GAAGGAAGCAGAGAACTTGGCCAAGGGGTCAACCATGCTGCTGACCAGGCTGGAAAGGAAGT
GGAGAAGCTTGGCCAAGGTGCCACCATGCTGCTGGCCAGGCCGGGAAGGAGCTGCAGAATGC
TCATAATGGGGTCAACCAAGCCAGCAAGGAGGCCAACCAGCTGCTGAATGGCAACCATCAAAG
CGGATCTTCCAGCCATCAAGGAGGGGCCACAACCACGCCGTTAGCCTCTGGGGCCTCAGTCAA
CACGCCTTTCATCAACCTTCCCGCCCTGTGGAGGAGCGTCGCCAACATCATGCCCCTAAACTGG
CATCCGGCCTTGCTGGGAGAATAATGTCGCCGTTGTCACATCAGCTGACATGACCTGGAGGGG
TTGGGGGTGGGGGACAGGTTTCTGAAATCCCTGAAGGGGGTTGTACTGGGATTTGTGAATAAA
CTTGATACACCA

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FIGURE 604

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA66675
><subunit 1 of 1, 247 aa, 1 stop
><MW: 25335, pI: 7.00, NX(S/T): 0
MHLARLVGSCSLLLLLGALSGWAASDDPIEKVIEGINRGLSNAEREVGKALDGINSGITHAGR
EVEKVFNGLSNMGSHTGKELDKGVQGLNHGMDKVAHEINHGIGQAGKEAEKLGHGVNNAAGQA
GKEADKAVQGFHTGVHQAGKEAEKLGQGVNHAADQAGKEVEKLGQGAHHAAGQAGKELQNAHN
GVNQASKEANQLLNGNHQSGSSSHQGGATTTPLASGASVNTPPFINLPALWRSVANIMP

Important features of the protein:

Signal peptide:

amino acids 1-25

Homologous region to circumsporozoite (CS) repeats:

amino acids 35-225

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FIGURE 605

GCGACGCGCGGGCGGGGCGGGCGAGAGGAAACGCGGGCGCCGGGGCCGGGCCCCGGCCCTGGAGATGG
TCCCCGGCGCCGCGGGGCTGGTGTGTCTCGTGCTCTGGCTCCCCGCGTGCGTCGCGGGCCCCACG
GCTTCCGTATCCATGATTATTTGTACTTTCAAGTGCTGAGTCCTGGGGACATTCGATACATCT
TCACAGCCACACCTGCCAAGGACTTTGGTGGTATCTTTCACACAAGGTATGAGCAGATTCACC
TTGTCCCCGCTGAACCTCCAGAGGCCTGCGGGGAACTCAGCAACGGTTTCTTCATCCAGGACC
AGATTGCTCTGGTGGAGAGGGGGGGCTGCTCCTTCCTCTCCAAGACTCGGGTGGTCCAGGAGC
ACGGCGGGCGGGCGGTGATCATCTCTGACAACGCAGTTGACAATGACAGCTTCTACGTGGAGA
TGATCCAGGACAGTACCCAGCGCACAGCTGACATCCCCGCCCTCTTCCTGCTCGGCCGAGACG
GCTACATGATCCGCCGCTCTCTGGAACAGCATGGGCTGCCATGGGCCATCATTTCCATCCCAG
TCAATGTCACCAGCATCCCCACCTTTGAGCTGCTGCAACCGCCCTGGACCTTCTGGTTAGAAAGA
GTTTGTCCCACATTCCAGCCATAAGTGACTCTGAGCTGGGAAGGGGAAACCCAGGAATTTTGC
TACTTGGAATTTGGAGATAGCATCTGGGGACAAGTGAGCCAGGTAGAGGAAAAGGGTTTGGG
CGTTGCTAGGCTGAAAGGGAAGCCACACCACTGGCCTTCCCTTCCCCAGGGCCCCCAAGGGTG
TCTCATGCTACAAGAAGAGGCAAGAGACAGGCCCCAGGGCTTCTGGCTAGAACCCGAAACAAA
AGGAGCTGAAGGCAGGTGGCCTGAGAGCCATCTGTGACCTGTCACACTCACCTGGCTCCAGCC
TCCCCTACCCAGGGTCTCTGCACAGTGACCTTCACAGCAGTTGTTGGAGTGGTTTAAAGAGCT
GGTGTTTGGGGACTCAATAAACCTCACTGACTTTTTAGCAATAAAGCTTCTCATCAGGGTTG
CAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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FIGURE 606

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA76532
><subunit 1 of 1, 188 aa, 1 stop
><MW: 21042, pI: 5.36, NX(S/T): 2
MVPGAAGWCCLVLWLPACVAAHGFRIDYLYFQVLSPGDIRYIFTATPAKDFGGIFHTRYEQI
HLVPAEPPEACGELSNGFFIQDQIALVERGGCSFLSKTRVVQEHGGRAVIISDNAVNDNSFYV
EMIQDSTQRTADIPALFLLGRDGYMIRRSLEQHGLPWAIISIPVNVTSIPTFELLQPPWTFW

Signal peptide:
amino acids 1-20

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FIGURE 607

GCATTTGCCACTGGTTGCAGATCAGGCGGACGAGGAGCCGGGAAGGCAGAGCC**ATG**TGGCTGC
CCCCTGCTCTGCTCCTTCTCAGCCTCTCAGGCTGTTTCTCCATCCAAGGCCAGAGTCTGTGA
GAGCCCCAGAGCAGGGGTCCCTGACGGTTCAATGCCACTATAAGCAAGGATGGGAGACCTACA
TTAAGTGGTGGTGCCGAGGGGTGCGCTGGGATACATGCAAGATCCTCATTGAAACCAGAGGGT
CGGAGCAAGGAGAGAAGAGTGACCGTGTGTCCATCAAGGACAATCAGAAAGACCGCACGTTCA
CTGTGACCATGGAGGGGCTCAGGCGAGATGACGCAGATGTTTACTGGTGTGGGATTGAAAGAA
GAGGACCTGACCTTGGGACTCAAGTGAAAGTGATCGTTGACCCAGAGGGAGCGGCTTCCACAA
CAGCAAGCTCACCTACCAACAGCAATATGGCAGTGTTTCATCGGCTCCCACAAGAGGAACCACT
ACATGCTCCTGGTATTTGTGAAGGTGCCCATCTTGCTCATCTTGGTCACTGCCATCCTCTGGT
TGAAGGGGTCTCAGAGGGTCCCTGAGGAGCCAGGGGAACAGCCTATCTACATGAACTTCTCCG
AACCTCTGACTAAAGACATGGCCACT**TAG**AGAGATGGATCTGCAGAGCCTTCCTGCCCTGGCC
ACGTTTCCAGAAGAGACTCGGGCTGTGGAAGGAACATCTACGAGTCCTCGGGATGCAGTGACT
GAGATAGGGGCCCTGGGCCCTCCGCCCTGGCCTTGGAGCTGGTGGGCACCTCCCTGTTCTGCAC
AGCTCAGGGACTTAGCCAGGTCTCTCCTGAGCCACCATCACCTCCTGGGGTGCCAGCACCTG
TTCTCTTGGTCAGGAGCTGTAGAGATGGAGCTCAAGCACTGGACGACTCTGTCCCCACTGCTG
GAATAACTCGGGCACAGAGCATGGGACCAAAGTACAGAAAGAGGTTGGGGGAGACCCCCCAG
CCCTAGACTTCCATCATTTCCGGAGACCAACTCAACACCGTCTTTGCCTGAGAACCTGATATATCC
GTGTTTTTAAATTTTTTTTTTTCTAGCAAAGTTGGGTTTTAATGACTTATGTTTCATAGGAAAC
CTCTCTGATCCCACACACAAGGAGGGTGATTCTGGGATGAGTTCCTGGTTCTAGGGCATGAGG
GGCTGGATGGACCCTGTCCCCAGGGAGGACATGGCTCTGAGTCCACAGGGCTGAGGAGGCAAT
GGGAACCTCCCTGGCCCCGGCCCGGTGCTTGTCCTCCCCCTCCCACCTCTTCCTCCTCCTAGCT
CCCCAAGCTCCCTGCCTATTTCCCCACCTCCGAGGGGCTGCAGCTTGGGAGCCTCCTCAGCAT
GACAGCTTGGGTCTCCTCCCCAAAAGAGCCTGTGAGGCCTCAAGAACCACCTCCAGGTGGGGA
GGGCAGTAACGAAAACCATCGCAGGAAATGGCACCTCCCTTTTCGGTGATGTTGAAATCATG
TTACTAATGAAAACCTGTCCTAGGGAAGTGTTCTGTCTCCTCACAGGCTTCACCCACGGCGAT
GAGGCCCTTGAATGTGGTCACTTTGTGCTGTATGGTTGAGGGACCCTCACACCAAAGGGACCT
TCCCATGTGAGATGTGCTCCCGCCCCCACCTGCCCAAGCAAACACACCACACATGTTCCGGC
ATGTTGCCCTTTGAACACCCATGAGGACGCCTCCAACCTGCTCTTGGTTCTAATAGGGAGTAC
TGACTGTCAGCAGTGGATAAAGGAGAGGGGACCCTCTGGTCCCTAGCATGGCACCCAGAGCCT
CCCCTCTTCTTGTCTTCAGCCAAAGAGAACTTTCTCTGACTTTGAACTGAATTTAGGTCTC
TGGCCAATGATGGGCCTGAAAATTCCATAATGGCCAGAGAGGAGAGTTTCGAGCCCCGGCTAAGA
TCCCCTGAGTCATTCTGTGAGGGACCAAGACCCACAGTCCACCAGCCCCAGGGCCCTACCTCC
TGGAATGCTTTCCTGGATCCAGCTTCCCGAAGATCCGACCAGACCCAGGGAGGACGGCACCGC
TCCGCGGGAGGGAAAGCCAAAGCATGGTGCTTACCAGCTGGACTCAGGGGCGAGGGGACATG
GGCGCTTGTCAACGTGATGTCATTCTTTTCCCACCGTTTCTTCCTGTTGATATTCAATGAATC
CGTCAATCTCTCTGGGAAA

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FIGURE 608

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105849
><subunit 1 of 1, 201 aa, 1 stop
><MW: 22689, pI: 7.41, NX(S/T): 1
MWLPPALLLLSLSGCFSIQGPESVRAPEQGSLTVQCHYKQGWETIYIKWWCRGVRWDTCKI
LIETRGSEQGEKSDRVSIKDNQKDRTFTVTMEGLRRDDADVWCGIERRGPD LGTQVKVI
VDPEGAASTTASSPTNSNMAVFIGSHKRNHMYLLVFVKVPILLILVTAILWLKGSQRVPE
EPGEQPIYMNFS EPLTKDMAT
```

Important features of the protein:**Signal peptide:**

Amino acids 1-17

Transmembrane domain:

Amino acids 151-170

N-glycosylation site:

Amino acids 190-194

Tyrosine kinase phosphorylation site:

Amino acids 95-103

N-myristoylation sites:

Amino acids 66-72;125-131

Prokaryotic membrane lipoprotein lipid attachment site:

Amino acids 5-16

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FIGURE 609

GATGGCGCAGCCACAGCTTCTGTGAGATTCTGATTTCTCCCCAGTTCCCCTGTGGGTCTGAGGG
GACCAGAAGGGTGAGCTACGTTGGCTTTCTGGAAGGGGAGGCTATATGCGTCAATTCCCCAAA
ACAAGTTTTGACATTTCCCCTGAAATGTCATTCTCTATCTATTCACTGCAAGTGCCTGCTGTT
CCAGGCCTTACCTGCTGGGCACTAACGGCGGAGCCAGGATGGGGACAGAATAAAGGAGCCACG
ACCTGTGCCACCAACTCGCACTCAGACTCTGAACCTCAGACCTGAAATCTTCTCTTCACGGGAG
GCTTGGCAGTTTTTCTTACTCCTGTGGTCTCCAGATTTCAAGCCTAAGATGAAAGCCTCTAGT
CTTGCCCTTCAGCCTTCTCTCTGCTGCGTTTTATCTCCTATGGACTCCTTCCACTGGACTGAAG
ACACTCAATTTGGGAAGCTGTGTGATCGCCACAAACCTTCAGGAAATACGAAATGGATTTTTCT
GAGATACGGGGCAGTGTGCAAGCCAAAGATGGAAACATTGACATCAGAATCTTAAGGAGGACT
GAGTCTTTGCAAGACACAAAGCCTGCGAATCGATGCTGCCTCCTGCGCCATTTGCTAAGACTC
TATCTGGACAGGGTATTTAAAACTACCAGACCCCTGACCATTATACTCTCCGGAAGATCAGC
AGCCTCGCCAATTCCTTTCTTACCATCAAGAAGGACCTCCGGCTCTCTCATGCCCACATGACA
TGCCATTGTGGGGAGGAAGCAATGAAGAAATACAGCCAGATTCTGAGTCACTTTGAAAAGCTG
GAACCTCAGGCAGCAGTTGTGAAGGCTTTGGGGGAACTAGACATTCTTCTGCAATGGATGGAG
GAGACAGAAATAGGAGGAAAGTGATGCTGCTGCTAAGAATATTCGAGGTCAAGAGCTCCAGTCT
TCAATACCTGCAGAGGAGGCATGACCCCAAACCACCATCTCTTACTGTACTAGTCTTGTGCT
GGTCACAGTGTATCTTATTTATGCATTACTTGCTTCCTTGCAATGATTGTCTTTATGCATCCCC
AATCTTAATTGAGACCATACTTGTATAAGATTTTTGTAAATATCTTCTGCTATTGGATATATT
TATTAGTTAATATATTTATTTATTTTTTGCTATTTAATGTATTTATTTTTTTACTTGGACATG
AACTTTAAAAAAATTCACAGATTATATTTATAACCTGACTAGAGCAGGTGATGTATTTTTAT
ACAGTAAAAAAAACCTTGTAATTCTAGAAGAGTGGCTAGGGGGGTATTTCATTTGTAT
TCAACTAAGGACATATTTACTCATGCTGATGCTCTGTGAGATATTTGAAATTGAACCAATGAC
TACTTAGGATGGGTGTGGAATAAGTTTTGATGTGGAATTGCACATCTACCTTACAATTACTG
ACCATCCCCAGTAGACTCCCCAGTCCCATAATTGTGTATCTTCCAGCCAGGAATCCTACACGG
CCAGCATGTATTTCTACAAATAAAGTTTTCTTGCATACCAAAAAAAAAAAAAAAAAAAAAA

615/615

FIGURE 610

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83500
><subunit 1 of 1, 261 aa, 1 stop
><MW: 29667, pI: 8.76, NX(S/T): 0
MRQFPKTSFDISPEMSFSIYSLQVPAVPGLTCWALTAEPGWGQNKGATTCATNSHSDSEL
RPEIFSSREAWQFFLLWSPDFRPKMKASSLAFSLLSAAFYLLWTPSTGLKTLNLGSCVI
ATNLQEIRNGFSEIRGSVQAKDGNIDIRILRRTESLQDTKPANRCCLLRHLLRLYLDRVF
KNYQTPDHYTLRKISSLANSEFLTIKKDLRLSHAHMTCHCGEEAMKKYSQILSHFEKLEPQ
AAVVKALGELDILLQWMEETE

Important features of the protein:**Signal peptide:**

Amino acids 1-42

cAMP- and cGMP-dependent protein kinase phosphorylation sites:

Amino acids 192-196;225-229

N-myristoylation sites:

Amino acids 42-48;46-52;136-142